

STIC-Biotech/ChemLib

167257

From: Yu, Misook
Sent: Thursday, September 29, 2005 9:19 AM
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Please do Interference search only for SEQ ID NO:2, and DNA encoding SEQ ID NO:1

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SEP 29 2005

BIO/CHM DIVISION
(STIC)

Searcher: Gan
Searcher Phone: 22504
Date Searcher Picked up: 10/3/05
Date completed: 10/3/05
Searcher Prep Time: 16
Online Time: 10

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: /
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: /
WWW/Internet: _____
Other (Specify): _____

Result No.	Score	Query	Match	Length	DB ID	Description
1	2816	100.0	2816	3	US-09-643-597-333	Sequence 333, App
2	2816	100.0	2816	4	US-09-542-615A-333	Sequence 333, App
3	2816	100.0	2816	4	US-09-606-121B-333	Sequence 333, App
4	2816	100.0	2816	4	US-09-630-940B-333	Sequence 333, App
5	2798	99.4	2810	4	US-09-049-016-5447	Sequence 544, App
6	13736	50.9	25679	4	US-09-943-016-17189	Sequence 1719, A
7	13736	48.9	2270	3	US-09-643-597-332	Sequence 332, App
8	13736	48.9	2270	4	US-09-542-615A-332	Sequence 332, App
9	13736	48.9	2270	4	US-09-606-121B-332	Sequence 332, App
10	13736	48.9	2270	4	US-09-630-940B-332	Sequence 332, App
11	1364	48.4	4849	3	US-09-643-597-335	Sequence 335, App
12	1364	48.4	4849	4	US-09-542-615A-335	Sequence 335, App
13	1364	48.4	4849	4	US-09-606-121B-335	Sequence 335, App
14	1364	48.4	4849	4	US-09-630-940B-335	Sequence 335, App
15	1232	43.8	1551	3	US-09-643-597-337	Sequence 337, App
16	1232	43.8	1551	4	US-09-542-615A-337	Sequence 337, App
17	1232	43.8	1551	4	US-09-606-121B-337	Sequence 337, App
18	1232	43.8	1551	4	US-09-940B-337	Sequence 337, App
19	1031	36.6	2082	3	US-09-643-597-334	Sequence 334, App
20	1031	36.6	2082	4	US-09-277-116-1	Sequence 1, Appl
21	1031	36.6	2082	4	US-09-542-615A-334	Sequence 334, App
22	1031	36.6	2082	4	US-09-606-121B-334	Sequence 334, App
23	1031	36.6	2082	4	US-09-630-940B-334	Sequence 334, App
24	1028	36.5	1386	3	US-09-643-597-336	Sequence 336, App
25	1028	36.5	1386	4	US-09-542-615A-336	Sequence 336, App
26	1028	36.5	1386	4	US-09-606-121B-336	Sequence 336, App
27	1028	36.5	1386	4	US-09-630-940B-336	Sequence 336, App

Qy	1381	CTTTCACCCCTGCTTCAAGAATGAGCTTGAGGCCGGAGAAACTCCAAAACATCT	1440	Db	2461	CTGATACTGTTCAGTCAGTCATTAGCCAGGAGCTAACGTTTGAGTAAGTCAAGC	2520		
Ds	1381	CTTTCACCCCTGCTTCAAGAATGAGCTTGAGGCCGGAGAAACTCCAAAACATCT	1440	Qy	2521	AGACCTGTTAAATGAGCTTCCCGACTCGAAATTAAAGATTGAAAGGTAGACTACTT	2580		
Qy	1441	GACGTCTCTTTAGACATTCGAAGCCCCAAACCGATCAAGTGTACCATAGGCCCTTC	1500	Db	2521	AGACCTGTTAAATGAGCTTCCCGACTCGAAATTAAAGATTGAAAGGTAGACTACTT	2580		
Ds	1441	GACGTCTCTTTAGACATTCGAAGCCCCAAACCGATCAAGTGTACCATAGGCCCTTC	1500	Qy	2581	TCTTTTTTACCAAGGAAATGAGAAATCTCCATTTCATTTAAAGCATATT	2640		
Qy	1501	TCTATATTAAAGTGTGTGTATTCCATGTTATGAGTTAGAGAACTTAAAGATATT	1560	Db	2581	TCTTTTTTACCAAGGAAATGAGAAATCTCCATTTCATTTAAAGCATATT	2640		
Ds	1501	TCTATATTAAAGTGTGTGTATTCCATGTTATGAGTTAGAGAACTTAAAGATATT	1560	Qy	2581	TTAGAGAAATGAGAAATCTCCATTTCATTTAAAGCATATT	2700		
Qy	1561	TGTGTGCGGTGTATCTAGCCCTATAAACAGGACTTGAGAAACTTGGCTAGAGA	1620	Db	2641	TTAACATAATAGCATTAAGACTTAAAGCTTAAAGATTTGAGAACTTCCCACCCAGT	2700		
Ds	1561	TGTGTGCGGTGTATCTAGCCCTATAAACAGGACTTGAGAAACTTGGCTAGAGA	1620	Db	2641	TTAACATAATAGCATTAAGACTTAAAGCTTAAAGATTTGAGAACTTCCCACCCAGT	2700		
Qy	1621	CCAACTGCTCAAAGCCAAGGCCACTAGTGAGAAATCTTTGAAGGAACTTAACT	1680	Db	2701	CACCGCACGTGATTTCGTCAGTCACCAAGAGAAATTTCTGTTGAGGCTGTGCRT	2760		
Ds	1621	CCAACTGCTCAAAGCCAAGGCCACTAGTGAGAACTTAACTTTGAAGGAACTTAACT	1680	Db	2701	CACCGCACGTGATTTCGTCAGTCACCAAGAGAAATTTCTGTTGAGGCTGTGCRT	2760		
Qy	1681	TTACAAGAAAGGATGTTCTCGAGATTGTTATCCTTAGACCGCCCATGGGGTGTAG	1740	Qy	2761	TTGGTGTGTTGTTGATTTGAGTTTATTTGAGAACTTTCATAACTTTCGATTTG	2816		
Ds	1681	TTACAAGAAAGGATGTTCTCGAGATTGTTATCCTTAGACCGCCCATGGGGTGTAG	1740	Db	2761	TTGGTGTGTTGATTTGAGTTTATTTGAGAACTTTCATAACTTTCGATTTG	2816		
Qy	1741	GAACCACTGTTGCTGAGCTTCTGTTGAGGGAGGGTCAAGTGGG	1800	RESULT 3					
Ds	1741	GAACCACTGTTGCTGAGCTTCTGTTGAGGGAGGGTCAAGTGGG	1800	<i>method w/ 10</i>					
Qy	1801	GAAAGGGGCAATTAGAGTTATTGAAACCCTTTCTGCTCTCTGTTCTAA	1860	Db	Sequence 3.3.3.1	US/09606421B			
Ds	1801	GAAAGGGGCAATTAGAGTTATTGAAACCCTTTCTGCTCTCTGTTCTAA	1860	Patent No.	6531315				
Qy	1861	AATTACACGGGAGCTTGGACGGGCTCAAACTTAAGATGTCCTTTAGAAAGGAG	1920	Qy	GENERAL INFORMATION:				
Ds	1861	AATTACACGGGAGCTTGGACGGGCTCAAACTTAAGATGTCCTTTAGAAAGGAG	1920	Applicant:	Wang, Tongtong				
Qy	1921	AAAAAAGTGTGTTATTGCTGCTGCTATAGGTTGAGGAACTGAGACTCAGTCAGA	1980	Applicant:	Fan, Lijun				
Ds	1921	AAAAAAGTGTGTTATTGCTGCTGCTATAGGTTGAGGAACTGAGACTCAGTCAGA	1980	Applicant:	Kalos, Michael D.				
Qy	1981	CCCTTTTAATGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2040	Applicant:	Banour, Chaitanya S.				
Ds	1981	CCCTTTTAATGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2040	Applicant:	Hosner, Nancy				
Qy	2041	TACTGTGGCGACGGCTACTACATTGCTGCTGCTGCTGCTGCTGCTGCTG	2100	Applicant:	Panger, Gary R.				
Ds	2041	TACTGTGGCGACGGCTACTACATTGCTGCTGCTGCTGCTGCTGCTGCTG	2100	Applicant:	Li, Samuel X.				
Qy	2101	TTTGTGAGAACTTGCAATTATGTTGCTCCCTCATGTTGAGGAACTTTCTTAAT	2160	Applicant:	Wang, Ajun				
Ds	2101	TTTGTGAGAACTTGCAATTATGTTGCTCCCTCATGTTGAGGAACTTTCTTAAT	2160	Applicant:	Skeiky, Yasir A.W.				
Qy	2161	GCTGTGTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2220	Title of Invention:	COMPOSITIONS AND METHODS FOR THE THERAPY				
Ds	2161	GCTGTGTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2220	Title of Invention:	AND DIAGNOSIS OF LUNG CANCER				
Qy	2221	CATGAAACCTGGAAAGACTACTACAAAACACTTGTGCTGCTGCTGCTGCTG	2280	File Reference:	1012145SC9				
Ds	2221	CATGAAACCTGGAAAGACTACTACAAAACACTTGTGCTGCTGCTGCTGCTG	2280	Current Application Number:	US/09/606,421B				
Qy	2281	CTCATTTGCTTAAATAGAAAGCAATCCACCCGTAATTTGCCCTTAGTTGAGTGT	2340	Current Filing Date:	2000-06-28				
Ds	2281	CTCATTTGCTTAAATAGAAAGCAATCCACCCGTAATTTGCCCTTAGTTGAGTGT	2340	Number of SEQ ID NOS:	358				
Qy	2341	TGTTAACATTAACTAAAGCTCAAAATCCACCCGTAATTTGCCCTTAGTTGAGTGT	2400	Software:	FastSeq for Windows Version 3.0				
Ds	2341	TGTTAACATTAACTAAAGCTCAAAATCCACCCGTAATTTGCCCTTAGTTGAGTGT	2400	SEQ ID NO:	333				
Qy	2401	AATTGGTGTAAATTAGACCTTCATCCCTAACGCCCATATTA	2460	Length:	2816				
Ds	2401	AATTGGTGTAAATTAGACCTTCATCCCTAACGCCCATATTA	2460	Query Match:	100.0%	Score: 2816;	DB: 4;	Length: 2816;	
Qy	2461	CCAGGGTTTCCACCATATCTGGACAGCTTATGTCAGTCAGTCAGCCC	2520	Best Local Similarity:	100.0%	Pred. No.: 0;	Mismatches: 0;	Indels: 0;	Gaps: 0;
Ds	2461	CCAGGGTTTCCACCATATCTGGACAGCTTATGTCAGTCAGTCAGCCC	2520	Matches 2816:	Conservative	0;			
Qy	2521	1 TCGTGTATCAAGACAGTGTGAGCATCCATTGAAACTTCACGTTGCGCACCC	60	Qy	1 TCGTGTATCAAGACAGTGTGAGCATCCATTGAAACTTCACGTTGCGCACCC	60			
Ds	2521	1 TCGTGTATCAAGACAGTGTGAGCATCCATTGAAACTTCACGTTGCGCACCC	60	Db	1 ACAGTACTGCCTGACCCATTACATTCAGGCTTCCTAGAACCCGGCTCATTTCTCTGG	120			
Qy	2581	TTCTTTTTACCAAGGAACTTCAACCTTCCATGTTGAGTGTGCTGCTGCTG	120	Qy	61 ACAGTACTGCCTGACCCATTACATTCAGGCTTCCTAGAACCCGGCTCATTTCTCTGG	120			
Ds	2581	TTCTTTTTACCAAGGAACTTCAACCTTCCATGTTGAGTGTGCTGCTGCTG	120	Db	61 ACAGTACTGCCTGACCCATTACATTCAGGCTTCCTAGAACCCGGCTCATTTCTCTGG	120			
Qy	2641	TTAACATAATAGCATTAAGACTAAAGCTTAAAGCTTCAACCTTCCATGCTGCTG	120	Qy	121 AAAGAAAGTTTACATGGCTTACCCATTGCTGCTGCTGCTGCTGCTG	180			
Ds	2641	TTAACATAATAGCATTAAGACTAAAGCTTAAAGCTTCAACCTTCCATGCTGCTG	120	Db	121 AAAGAAAGTTTACATGGCTTACCCATTGCTGCTGCTGCTGCTGCTG	180			
Qy	2700	TTGGTGTGTTGTTGAGGCTTCTGTTGAGGCTTCTGTTGAGGCTTCTGTTG	2700	Qy	181 CCAGGGTTTCCACCATATCTGGACAGCTTATGTCAGTCAGTCAGCCC	240			
Ds	2700	TTGGTGTGTTGTTGAGGCTTCTGTTGAGGCTTCTGTTGAGGCTTCTGTTG	2700	Db	181 CCAGGGTTTCCACCATATCTGGACAGCTTATGTCAGTCAGTCAGCCC	240			
Qy	2761	TTGGTGTGTTGTTGAGGCTTCTGTTGAGGCTTCTGTTGAGGCTTCTGTTG	2761	Qy	241 ATTGGTGTGACTTGTGCAATTAGGCTTACGTTGAGGAGCTTACGTTGAGATCCAGC	300			

Db	241	AATGACTGTGAACATTGGGATGAACTCATGAGAATCGGACCAAAAGATTGAGATT	Qy	1381	CTTTCAGCCCTGCTTCAGGAATGAGCTTGTGGAGCCCCATGTGGCACAGTAC	1440
301	AGCATGGACTGTATCCGATGGAGGACTCGGACCTGTGAGTGGCCACAGTAC	Db	1381	CTTTCAGCCCTGCTTCAGGAATGAGCTTGTGGAGCCCCATGTGGCACAGTAC	1440	
301	AGCATGGACTGTATCCGATGGAGGACTCGGACCTGTGAGTGGCCACAGTAC	Db	1381	CTTTCAGCCCTGCTTCAGGAATGAGCTTGTGGAGCCCCATGTGGCACAGTAC	1440	
361	AGAACCTGGGGTCTCTGAAAGCATGGACCGAGATTCAAACCGCTCTGTGCCACC	Qy	1441	GACGTCTCTTGTAGCTTCAAGCCCCAACCCATAGGCCATAGGCCATAGGCCATAG	1500	
361	AGAACCTGGGGTCTCTGAAAGCATGGACCGAGATTCAAACCGCTCTGTGCCACC	Db	1441	GACGTCTCTTGTAGCTTCAAGCCCCAACCCATAGGCCATAGGCCATAGGCCATAG	1500	
421	AGTCCCTATAACACAGACCCACCGCAGAACGGTCAAGGCCCTTGCCCTAGCACAG	Qy	1501	TCTATATTAAAGTGTGTGTATATGTGATATGTGATATGTGATATGTGATATGTGAT	1560	
421	AGTCCCTATAACACAGACCCACCGCAGAACGGTCAAGGCCCTTGCCCTAGCACAG	Db	1501	TCTATATTAAAGTGTGTGTATATGTGATATGTGATATGTGATATGTGATATGTGAT	1560	
481	CCCAGCTCCACCTTCGATGCTCTCTCCATACCCGCCATACCCCTCCAACACCGACTAC	Qy	1561	TGTGTGCGCTGTGTATCTAGCCCTTAAGAGACTTGTGATCTAGCCCTAAGAGA	1620	
481	CCCAGCTCCACCTTCGATGCTCTCTCCATACCCCTCCAACACCGACTAC	Db	1561	TGTGTGCGCTGTGTATCTAGCCCTTAAGAGACTTGTGATCTAGCCCTAAGAGA	1620	
541	CGAGGCCAGTCAAGGCAAGGGCAAGTGGCAAGCGCCAAAGTGGGCCACC	Qy	1621	CCCAACTGCTCAAGGCAAAAGCCACTACAGGAGATCTTGTGATCTAGCCCTAAGAGA	1680	
541	CGAGGCCAGTCAAGGCAAGGGCAAGTGGCAAGCGCCAAAGTGGGCCACC	Db	1621	CCCAACTGCTCAAGGCAAAAGCCACTACAGGAGATCTTGTGATCTAGCCCTAAGAGA	1680	
601	TGGACGTATTCCACTGAACTGAAAGAAACTCTACTGCCCCAAAGTCAAGACATGCCCATC	Qy	1681	TTACAAAGAAAGGATGTTTTCGAGATTTGTGATCTCTAGCCGGCATGGGTGAG	1740	
601	TGGACGTATTCCACTGAACTGAAAGAAACTCTACTGCCCCAAAGTCAAGACATGCCCATC	Db	1681	TTACAAAGAAAGGATGTTTTCGAGATTTGTGATCTCTAGCCGGCATGGGTGAG	1740	
661	CAGATCAGGTATGACCCCAACTCTAGGGAGCTTATCCGGCCCATGCCGTCTAC	Qy	1741	GAACCACTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1800	
661	CAGATCAGGTATGACCCCAACTCTAGGGAGCTTATCCGGCCCATGCCGTCTAC	Db	1741	GAACCACTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1800	
721	AAAAAAGCTGACCGTCAGBGGGTTGAGGGTCCAAACCATGAGTGTGACCGT	Qy	1801	GAAGGGCCATTAAAGATGTTTATTGGAACCCCTTTCTGTCCTCTCTCTCTCTCTCT	1860	
721	AAAAAAGCTGACCGTCAGBGGGTTGAGGGTCCAAACCATGAGTGTGACCGT	Db	1801	GAAGGGCCATTAAAGATGTTTATTGGAACCCCTTTCTGTCCTCTCTCTCTCTCT	1860	
781	GAATTCAACGAGGGCAGATTCGGGAGCTGGTGGAAAGCAGC	Qy	1861	AATTCAACGAGGGCTTGGCAGGGTCAAAACTTAAGATGTCCTTTTAAGAAAGAG	1920	
781	GAATTCAACGAGGGCAGATTCGGGAGCTGGTGGAAAGCAGC	Db	1861	AATTCAACGAGGGCTTGGCAGGGTCAAAACTTAAGATGTCCTTTTAAGAAAGAG	1920	
841	CATGCCCTAGTGTAGAGATGCCATACAGGAAGACAGTGTGGTACCTTATGAG	Qy	1921	AAAAAAACTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1980	
841	CATGCCCTAGTGTAGAGATGCCATACAGGAAGACAGTGTGGTACCTTATGAG	Db	1921	AAAAAAACTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1980	
901	CTACCCCTGGGACTGCTGGTGGAACTCTGTTGCTGCTGCTGCTGCTGCTGCTGCTG	Qy	1981	CCCTTTAAATGTGGCTCATGTAATAATGTCAGTGTGAACTTGGGGTGGAGTCT	2040	
901	CTACCCCTGGGACTGCTGGTGGAACTCTGTTGCTGCTGCTGCTGCTGCTGCTG	Db	1981	CCCTTTAAATGTGGCTCATGTAATAATGTCAGTGTGAACTTGGGGTGGAGTCT	2040	
961	TCTGTTGGAGGGTATGAACTGCTGGCTCCAAATTCTGAAACCTGAGT	Qy	2041	TACTGTGGAGCGAGGTGATCTTACAAAGTAACTTGGGGTGGAGTCT	2100	
961	TCTGTTGGAGGGTATGAACTGCTGGCTCCAAATTCTGAAACCTGAGT	Db	2041	TACTGTGGAGCGAGGTGATCTTACAAAGTAACTTGGGGTGGAGTCT	2100	
961	TGTGTGAGGGATGAACTGCTGGCTCCAAATTCTGAAACCTGAGT	Qy	2101	TTTGTTGAAACTGTGCTTGTGCTCCCTCATGTTGAGGTAACTTCTTAAT	2160	
1021	GGGCAAGTCTGGCCGAGCTGCTGGCTTGTGGCCGGATCTGGCCGGATCTGGCTGG	Qy	2101	TTTGTTGAAACTGTGCTTGTGCTCCCTCATGTTGAGGTAACTTCTTAAT	2160	
1021	GGGCAAGTCTGGCCGAGCTGCTGGCTTGTGGCCGGATCTGGCTGG	Db	2101	TTTGTTGAAACTGTGCTTGTGCTCCCTCATGTTGAGGTAACTTCTTAAT	2160	
1141	CATGGTAGCAAGCAGCCGGTCAAGCATGAGTGGCAAGAACAGGGT	Qy	2161	GCTGCTGAACTGGCCACTGTGGCATGTTATGCTAAAGTTTCTGTGTA	2220	
1141	CATGGTAGCAAGCAGCCGGTCAAGCATGAGTGGCAAGAACAGGGT	Db	2161	GCTGCTGAACTGGCCACTGTGGCATGTTATGCTAAAGTTTCTGTGTA	2220	
1081	AGGAAGGGGATGAACTGCTGGCTCCAAATTCTGAAACCTGAGT	Qy	2221	CATGAAACCTGGAGAGCTACTACAAAAACTGTGTTGGCCCATAGGGCTAA	2280	
1081	AGGAAGGGGATGAACTGCTGGCTCCAAATTCTGAAACCTGAGT	Db	2221	CATGAAACCTGGAGAGCTACTACAAAAACTGTGTTGGCCCATAGGGCTAA	2280	
1141	CATGGTAGCAAGCAGCCGGTCAAGCATGAGTGGCAAGAACAGGGT	Qy	2281	CTCATTTGTGGTTTAAATGAAAGGAACTTACCTCCCTAGTGTAGT	2340	
1141	CATGGTAGCAAGCAGCCGGTCAAGCATGAGTGGCAAGAACAGGGT	Db	2281	CTCATTTGTGGTTTAAATGAAAGGAACTTACCTCCCTAGTGTAGT	2340	
1081	AGGAAGGGGATGAACTGCTGGCTCCAAATTCTGAAACCTGAGT	Qy	2341	TGTTTACATTATTCAAGCTCAAATTAGAAATTGAAATTGAAATTGAAATTG	2400	
1081	AGGAAGGGGATGAACTGCTGGCTCCAAATTCTGAAACCTGAGT	Db	2341	TGTTTACATTATTCAAGCTCAAATTAGAAATTGAAATTGAAATTGAAATTG	2400	
1201	AAACGAAGAATCCCAGTGTAACTGCTTACCTTACCTGAGTGGCCGTGAGACTT	Qy	2401	AATTGGCTTAAATTAGAGCTTCTATCCCTCAAGCCCTACTACCTAAACCCGCTAT	2460	
1201	AAACGAAGAATCCCAGTGTAACTGCTTACCTTACCTGAGTGGCCGTGAGACTT	Db	2401	AATTGGCTTAAATTAGAGCTTCTATCCCTCAAGCCCTACTACCTAAACCCGCTAT	2460	
1321	ATTGAAACGTCACGGCAACAGCAACAGCAGCAACAGCAACATCTC	Qy	2461	ATTGAAACGTCACGGCAACAGCAACAGCAGCAACAGCAACATCTC	2460	
1321	ATTGAAACGTCACGGCAACAGCAACAGCAGCAACAGCAACATCTC	Db	2461	ATTGAAACGTCACGGCAACAGCAACAGCAGCAACAGCAACATCTC	2460	

2461	CTGATACTGTCAGTGCATTAGCCAGGAACTTACCTTTCAGTAGTGACATCCAGC	2520	Qy	241 ATTCACTGAACTTCCGATGCAAGACTGGACCTGACAAAGATGGATTGAGATT	300
Db	CTGATACTGTCAGTGCATTAGCCAGGAACTTACCTTTCAGTAGTGACATCCAGC	2520	Db	241 ATTCACTGAACTTCCGATGCAAGACTGGACCTGACAAAGATGGATTGAGATT	300
Qy	2521 AGACGTGTTAATACGACTCTGGACTGAAATTAAAGATTGAAAGGTGAGACTT	2580	Qy	301 AGCATGGACTGATCCGGATCGAACGACTGGACCTGACCCATGTCGCCACAGTAC	360
Db	2521 AGACGTGTTAATACGACTCTGGACTGAAATTAAAGATTGAAAGGTGAGACTT	2580	Db	301 AGCATGGACTGATCCGGATCGAACGACTGGACCTGACCCATGTCGCCACAGTAC	360
Qy	2581 TTCTTTTTTACTCAAAGTTAGAGAATCTCTGTTCCATTAAACACATAT	2640	Qy	361 ACGAAACCTGGGCTCTGAAACGATGGCTCTGTCGCCAC	420
Db	2581 TTCTTTTTTACTCAAAGTTAGAGAATCTCTGTTCCATTAAACACATAT	2640	Db	361 ACGAAACCTGGGCTCTGAAACGATGGCTCTGTCGCCAC	420
Qy	2641 TTAGATAATGCAAAAGACTTTAAATGTTCCCTCCCATCTTCCCACACCACT	2700	Qy	421 AGTCCCTATAACAGACCAAGGAAAGACAGCGTACCGGGCCTTACGGCAGAG 480	
Db	2641 TTAGATAATGCAAAAGACTTTAAATGTTCCCTCCCATCTTCCCACACCACT	2700	Db	421 AGTCCCTATAACAGACCAAGGAAAGACAGCGTACCGGGCCTTACGGCAGAG 480	
Qy	2701 CACCAAGACTGTATTTCTGACCAAGAACATGATTCTGTTATGGGTGTTCT	2760	Qy	481 CCCAGCTCAGCTTCCATCCCTCCATCCCCGATTCACCGGATTCACCCGAAAC 540	
Db	2701 CACCAAGACTGTATTTCTGACCAAGAACATGATTCTGTTATGGGTGTTCT	2760	Db	481 CCCAGCTCACCTTCGATGCTCTCTGATGCTCTCTGATGCTCTCTGATGCT 540	
Qy	2761 TTGTGGATGTTGATTTAATTTCATAAAACTTTGACATCTGGTTAAAGAAA	2816	Qy	541 CCAGGGCGCACAGTTTGACAGTGTCTTCAGGATGTCGAGCACCAGC 600	
Db	2761 TTGTGGATGTTGATTTAATTTCATAAAACTTTGACATCTGGTTAAAGAAA	2816	Db	541 CCAGGGCGCACAGTTTGACAGTGTCTTCAGGATGTCGAGCACCAGC 600	
Qy	601 TGGAAGTTTCCACTGAAAGAACTCTACTGCAATTTGCAAAATGGCCATC	660	Qy	601 TGGAAGTTTCCACTGAAAGAACTCTACTGCAATTTGCAAAATGGCCATC	660
Db	601 TGGAAGTTTCCACTGAAAGAACTCTACTGCAATTTGCAAAATGGCCATC	660	Db	601 TGGAAGTTTCCACTGAAAGAACTCTACTGCAATTTGCAAAATGGCCATC	660
Qy	661 CAGATCAAGGTGATGACCCACCTCTCAGGGAGCTGTATCGGGCCATCTGCT	720	Qy	661 CAGATCAAGGTGATGACCCACCTCTCAGGGAGCTGTATCGGGCCATCTGCT	720
Db	661 CAGATCAAGGTGATGACCCACCTCTCAGGGAGCTGTATCGGGCCATCTGCT	720	Db	661 CAGATCAAGGTGATGACCCACCTCTCAGGGAGCTGTATCGGGCCATCTGCT	720
Qy	721 AAAAAAGTGGACGTCACGGGGTGGTGAAGGGTGCCCAACATGAGCTGACCGT	780	Qy	721 AAAAAAGTGGACGTCACGGGGTGGTGAAGGGTGCCCAACATGAGCTGACCGT	780
Db	721 AAAAAAGTGGACGTCACGGGGACAGATGGCCCAACATGAGCTGACCGT	780	Db	721 AAAAAAGTGGACGTCACGGGGACAGATGGCCCAACATGAGCTGACCGT	780
Qy	781 GATTCAACGAGGAAACAGATTGCCCCCTAGTCAATTGTTGACCTTATGAG	900	Qy	781 GATTCAACGAGGAAACAGATTGCCCCCTAGTCAATTGTTGACCTTATGAG	900
Db	781 GATTCAACGAGGAAACAGATTGCCCCCTAGTCAATTGTTGACCTTATGAG	900	Db	781 GATTCAACGAGGAAACAGATTGCCCCCTAGTCAATTGTTGACCTTATGAG	900
Qy	841 CATGCCAGTATGTAAGAATCCATACAGGAAGACAGATGTTGACCTTATGAG	900	Qy	841 CATGCCAGTATGTAAGAATCCATACAGGAAGACAGATGTTGACCTTATGAG	900
Db	841 CATGCCAGTATGTAAGAATCCATACAGGAAGACAGATGTTGACCTTATGAG	900	Db	841 CATGCCAGTATGTAAGAATCCATACAGGAAGACAGATGTTGACCTTATGAG	900
Qy	901 CCACCCAGGTGGACACTGAATTCAAGGAACTGTTGACCTTATGAGCTGTT	960	Qy	901 CCACCCAGGTGGACACTGAATTCAAGGAACTGTTGACCTTATGAGCTGTT	960
Db	901 CCACCCAGGTGGACACTGAATTCAAGGAACTGTTGACCTTATGAGCTGTT	960	Db	901 CCACCCAGGTGGACACTGAATTCAAGGAACTGTTGACCTTATGAGCTGTT	960
Qy	961 TGTCTTGGGGATGAAAGGAACTTAAATCATGTTGACCTTATGAGCTGTT	102	Qy	961 TGTCTTGGGGATGAAAGGAACTTAAATCATGTTGACCTTATGAGCTGTT	102
Db	961 TGTCTTGGGGATGAAAGGAACTTAAATCATGTTGACCTTATGAGCTGTT	102	Db	961 TGTCTTGGGGATGAAAGGAACTTAAATCATGTTGACCTTATGAGCTGTT	102
Qy	1021 GGCGAAAGTCTGGCTCGAGCTGCTGCTGAGGCCGGATCTGTGCTGCTG	108	Qy	1021 GGCGAAAGTCTGGCTCGAGCTGCTGCTGAGGCCGGATCTGTGCTGCTG	108
Db	1021 GGCGAAAGTCTGGCTCGAGCTGCTGCTGAGGCCGGATCTGTGCTG	108	Db	1021 GGCGAAAGTCTGGCTCGAGCTGCTGCTGAGGCCGGATCTGTGCTG	108
Qy	1 TCGTGTGATATAAAAGAACAGTGTGAAAGGAAATGTTGAAACTTCAGGTGTGCCACCT	60	Qy	1081 AGGAGGGCGATGAGATGGCATGAAAGCAGCAATGGTATCCAGTAAAGAACGGT	114
Db	1 TCGTGTGATATAAAAGAACAGTGTGAAAGGAAATGTTGAAACTTCAGGTGTGCCACCT	60	Db	1081 AGGAGGGCGATGAGATGGCATGAAAGCAGCAATGGTATCCAGTAAAGAACGGT	114
Qy	61 ACAGTACTGCCCTGACCTTACATCCAGCTTGTGTTGAAACCCAGTCATTCTCTTG	120	Qy	1141 GATGGTACAAAGGCCGGTTCTGTTGAAACACAGCATGGTATCCAGTAAAGAACGGT	120
Db	61 ACAGTACTGCCCTGACCTTACATCCAGCTTGTGTTGAAACCCAGTCATTCTCTTG	120	Db	1141 GATGGTACAAAGGCCGGTTCTGTTGAAACACAGCATGGTATCCAGTAAAGAACGGT	120
Qy	121 AAAGAAAGTATTACCGATCCACCATGTCAGGAAATGTTGAAACTTCAGT	180	Qy	1201 AAACCAAGATCCCGAGATGAACTGCTGGAAACTCATGGTACTCTCTGAGCACACA	132
Db	121 AAAGAAAGTATTACCGATCCACCATGTCAGGAAATGTTGAAACTTCAGT	180	Db	1201 AAACCAAGATCCCGAGATGAACTGCTGGAAACTCATGGTACTCTCTGAGCACACA	132
Qy	181 CGAGAGTTTCAGATATCTGGATTCAGGAACTGTTCTGAGACGGCTTATGAGCTT	240	Qy	1261 GAAATGCTTGTGAGATAAAAGCTGCCCTTATGAGCTTCTCTGAGCACACA	132
Db	181 CGAGAGTTTCAGATATCTGGATTCAGGAACTGTTCTGAGACGGCTTATGAGCTT	240	Db	1261 GAAATGCTTGTGAGATAAAAGCTGCCCTTATGAGCTTCTCTGAGCACACA	132

QY 1321 ATTTAAAGTACGGCAACGCCAACGAGCACACCCGACTTACCTCAGAACATTC 1380
 Db 1321 ATTTAAAGTACGGCAACGCCAACGAGCACACCCGACTTACCTCAGAACATTC 1380
 QY 1381 CTTTCAGCTGCTTCAGAAATGAGCTTGTGAGCCCGAGAGAAAATCCTAACATCTC 1380
 Db 1381 CTTTCAGCTGCTTCAGAAATGAGCTTGTGAGCCCGAGAGAAAATCCTAACATCTC 1380
 QY 1440 GAGCTCTTCTTGTAGACATTCAAGCCCCAACCGATACTGTACCCATAGAGCCCTATC 1440
 Db 1440 GAGCTCTTCTTGTAGACATTCAAGCCCCAACCGATACTGTACCCATAGAGCCCTATC 1440
 QY 1441 GAGCTCTTCTTGTAGACATTCAAGCCCCAACCGATACTGTACCCATAGAGCCCTATC 1500
 Db 1441 GAGCTCTTCTTGTAGACATTCAAGCCCCAACCGATACTGTACCCATAGAGCCCTATC 1500
 QY 1441 GAGCTCTTCTTGTAGACATTCAAGCCCCAACCGATACTGTACCCATAGAGCCCTATC 1500
 Db 1441 GAGCTCTTCTTGTAGACATTCAAGCCCCAACCGATACTGTACCCATAGAGCCCTATC 1500
 QY 1501 TCTATATTTTAAGTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1560
 Db 1501 TCTATATTTTAAGTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1560
 QY 1561 TGTGTGCGGT 1620
 Db 1561 TGTGTGCGGT 1620
 QY 1621 CCCAACTGCTCAAAGGCCAACCCACTAGTGAGAGATCTTGTGAGCTAACAGGCT 1680
 Db 1621 CCCAACTGCTCAAAGGCCAACCCACTAGTGAGAGATCTTGTGAGCTAACAGGCT 1680
 QY 1681 TTACAAGAAGGATGTTTCAGACGGCATTGTGTTGGGTGAG 1740
 Db 1681 TTACAAGAAGGATGTTTCAGACGGCATTGTGTTGGGTGAG 1740
 QY 1741 GAAACCCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1800
 Db 1741 GAAACCCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1800
 QY 1801 GAAAGGGGCATTAAGATGTTTATGGAAACCTTTCTGTTGTTGTTGTTGTTGTTGTT 1860
 Db 1801 GAAAGGGGCATTAAGATGTTTATGGAAACCTTTCTGTTGTTGTTGTTGTTGTTGTT 1860
 QY 1861 AATTCAAGGGAAAGCTTCAAACTTAAAGTCTCTCTCTCTCTCTCTCTCTCTCT 1920
 Db 1861 AATTCAAGGGAAAGCTTCAAACTTAAAGTCTCTCTCTCTCTCTCTCTCTCTCTCT 1920
 QY 1921 AAAAAAGCTGTTTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1980
 Db 1921 AAAAAAGCTGTTTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1980
 QY 1981 CCCTTTTAATGCTGTCATGTTAAATAATTGCAACTAGTAGTAAAGGAGCTGTCAGTG 2040
 Db 1981 CCCTTTTAATGCTGTCATGTTAAATAATTGCAACTAGTAGTAAAGGAGCTGTCAGTG 2040
 QY 2101 TTTGTGAAACATTGCAATTATTGCAACTAGTAACTTGTGTTGGGGAGGTCT 2100
 Db 2101 TTTGTGAAACATTGCAATTATTGCAACTAGTAACTTGTGTTGGGGAGGTCT 2100
 QY 2101 TTTGTGAAACATTGCAATTATTGCAACTAGTAACTTGTGTTGGGGAGGTCT 2160
 Db 2101 TTTGTGAAACATTGCAATTATTGCAACTAGTAACTTGTGTTGGGGAGGTCT 2160
 QY 2161 GCTGTTGTAACCTGCTGCACTGTGTTGGCATCTGTTATGCTAAAGTTTCTGTGA 2220
 Db 2161 GCTGTTGTAACCTGCTGCACTGTGTTGGCATCTGTTATGCTAAAGTTTCTGTGA 2220
 QY 2221 CATGAAACCTGAAAGCCTACTACAAAAAAACTGTGTTGGCATCTGTTATGCTAAAGTT 2280
 Db 2221 CATGAAACCTGAAAGCCTACTACAAAAAAACTGTGTTGGCATCTGTTATGCTAAAGTT 2280
 QY 2281 CTCATTTGTCGTTTAAATGAAAGCRAATTCACCCCCAGTAATTCACCCCCAGTAATTCAC 2340
 Db 2281 CTCATTTGTCGTTTAAATGAAAGCRAATTCACCCCCAGTAATTCACCCCCAGTAATTCAC 2340
 QY 2341 TGTGTTACCATATTCAAAAGCTCAAATATGAAAGCCCTCTCACAATATCTCTGTTGATT 2400
 Db 2341 TGTGTTACCATATTCAAAAGCTCAAATATGAAAGCCCTCTCACAATATCTCTGTTGATT 2400
 QY 2401 ATTGTCGTTAAATTAGACCTCTTATCCCTCAAGCTTACCTACATAAACGCCCATATTA 2460

RESULT 5
 US-09-949-016-5447
 ; Sequence 5447, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949_016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIORITY NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-13
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: Fast-SEQ for Windows Version 4.0
 ; SEQ ID NO: 5447
 ; LENGTH: 2810
 ; TYPE: DNA
 ; ORGANISM: Human
 US-09-949-016-5447

Query Match 99.4%; Score 2798; DB 4; Length 2810;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2809; Conservative 0; Mismatches 1; Gaps 1;

QY 1 TCGTGTGTTATCAAGACAGTCAGGAAATGTTGAAATTCTCAGGTGTCGCCACCCCT 60
 Db 1 ACAGTATGCGCTGACCTTAATCGTGGCTGTTCTGTTGAAACTTCAGGTGTCGCCACCCCT 60
 QY 1 TCGTGTGTTATCAAGACAGTCAGGAAATGTTGAAATTCTCAGGTGTCGCCACCCCT 60
 Db 1 ACAGTATGCGCTGACCTTAATCGTGGCTGTTCTGTTGAAACTTCAGGTGTCGCCACCCCT 60
 QY 120 GAAAGAAAGTTTACCGATCCACCTGTCAGGAACTGAAATGTAATTCCCTCAG 179
 Db 61 ACAGTATGCGCTGACCTTAATCGTGGCTGTTCTGTTGAAACTTCAGGTGTCGCCACCCCT 60
 QY 61 GAAAGAAAGTTTACCGATCCACCTGTCAGGAACTGAAATGTAATTCCCTCAGGTGTCGCCACCCCT 60
 Db 61 ACAGTATGCGCTGACCTTAATCGTGGCTGTTCTGTTGAAACTTCAGGTGTCGCCACCCCT 60
 QY 180 TCCAGAGTTTCAGGATATGTTGTTCTGGAAAGCCCTATATGTTGTTCTGTTGAAACTTCAGGTGTCGCCACCCCT 219
 Db 181 TCCAGAGTTTCAGGATATGTTGTTCTGGAAAGCCCTATATGTTGTTCTGTTGAAACTTCAGGTGTCGCCACCCCT 240

QY

RESULT 7
US-09-643-597-332
; Sequence 332, Application US/09643597
; Patent No. 6,260,722

; GENERAL INFORMATION:
 ; APPLICANT: Wang, Tongtong
 ; APPLICANT: Fan, Liqun
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Bangur, Chaitanya S.
 ; APPLICANT: Hosken, Nancy
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Ajun
 ; APPLICANT: Skeity, Yasir A.W.
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: McNeill, Patricia D.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
 ; FILE REFERENCE: 21010121.455C11
 ; CURRENT APPLICATION NUMBER: US/09/643,597
 ; CURRENT FILING DATE: 2000-08-21
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 332
 ; LENGTH: 2270
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-643-597-332

Query Match 1376 Score 1376; DB 3; Length 2270;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1376; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTTGATATCAAAGACAGTTCAGGAATGAAATTGAAACTTCAAGGTGCCCCCT 60
 Db 1 TCGTTGATATCAAAGACAGTTCAGGAATGAAATTGAAACTTCAAGGTGCCCCCT 60
 Qy 61 ACAGTACTGCCCTGACCCCTTACATCCAGCGTTCAAGGAATGAAATTGAAACTTCAAGGTGCCCCCT 120
 Db 61 ACAGTACTGCCCTGACCCCTTACATCCAGCGTTCAAGGAATGAAATTGAAACTTCAAGGTGCCCCCT 120
 Qy 121 AAAGAAGTTTACCGATCCACCATGCCAGAACACAGAACAAATGAAATTCTCAGT 180
 Db 121 AAAGAAGTTTACCGATCCACCATGCCAGAACACAGAACAAATGAAATTCTCAGT 180
 Qy 181 CCAGAGSTTTCCAGATATCGGATTTCGGATTTCGGAAACAGCCATAATGTCAGTTCAGCC 240
 Db 181 CCAGAGSTTTCCAGATATCGGATTTCGGATTTCGGAAACAGCCATAATGTCAGTTCAGCC 240
 Qy 241 ATTGACTTGAACCTTGTGATGAAACATCAGAGATGTTGCGAACAAACAAATTGAGATT 300
 Db 241 ATTGACTTGAACCTTGTGATGAAACATCAGAGATGTTGCGAACAAACAAATTGAGATT 300
 Qy 301 ACCATGCACTGTATCCGATGCCAGGACTCGGACCTGAGTGAACCCCATGTCAGTAC 360
 Db 301 ACCATGCACTGTATCCGATGCCAGGACTCGGACCTGAGTGAACCCCATGTCAGTAC 360
 Qy 361 ACGAACCTGGGCTCTGAAACGATGACCGAGAACATGAGAACAAACGGCTCTCGTCACC 420
 Db 361 ACGAACCTGGGCTCTGAAACGATGACCGAGAACATGAGAACAAACGGCTCTCGTCACC 420
 Qy 421 AGTCCTATAACAGAACACGGCAACGCGCACAGCGTCAACGGCACAG 480

RESULT 8
US-09-670-568c-2.rni
; Sequence 332, Application US/09643597
; Patient No. 6518256
; GENERAL INFORMATION:
 ; APPLICANT: Wang, Tongtong
 ; APPLICANT: Fan, Liqun
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Bangur, Chaitanya S.

APPLICANT: Hosken, Nancy A.
 APPLICANT: Fanger, Gary R.
 TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
 FILE REFERENCE: 210121.455CB
 CURRENT APPLICATION NUMBER: US/09/542,615A
 CURRENT FILING DATE: 2000-04-14
 NUMBER OF SEQ ID NOS: 350
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 332
 LENGTH: 2270
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-542-615A-332

Query Match 1 TCGTTGATATCAAAGACAGTCAGGTCAAGGAATGAATTGAACTTCACGGTGTGCCAACCT 60
 Best Local Similarity 48.9%; Score 1376; DB 4; Length 2270;
 Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
 Matches 1376; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTTGATATCAAAGACAGTCAGGTCAAGGAATGAATTGAACTTCACGGTGTGCCAACCT 60
 Db 1 TCGTTGATATCAAAGACAGTCAGGTCAAGGAATGAATTGAACTTCACGGTGTGCCAACCT 60
 Qy 61 ACAGTACTGCCCTGACCCCTAACATCCAGCGTTCGPAAACCACGTCATTTCCTCTGG 120
 Db 61 ACAGTACTGCCCTGACCCCTAACATCCAGCGTTCGPAAACCACGTCATTTCCTCTGG 120
 Qy 121 AAAGAAAGTTTAATTACCGATTCACCATGTCAGAACAAATGAAATTCTCAGT 180
 Db 121 AAAGAAAGTTTAATTACCGATTCACCATGTCAGAACAAATGAAATTCTCAGT 180
 Qy 181 CCAGAGTTTCCAGCTATCTGGATTTCCTGAACTGCCTATACTGTTCTGCC 240
 Db 181 CCAGAGTTTCCAGCTATCTGGATTTCCTGAACTGCCTATACTGTTCTGCC 240
 Qy 241 ATTGACTTGAACTTTGGTGTGATTAACCATCAGAGATGTTGGCACAACAAAGATGGATT 300
 Qy 241 ATTGACTTGAACTTTGGTGTGATTAACCATCAGAGATGTTGGCACAACAAAGATGGATT 300
 Db 301 AGCATGAACTGTATGCCATGAGGACTGGACCTGAGTGAACGCCATGTCAC 360
 Db 301 AGCATGAACTGTATGCCATGAGGACTGGACCTGAGTGAACGCCATGTCAC 360
 Qy 361 AGAACCTGGGCTCTCTGAAAGCATGACCGAATCTGAAACGGCTCTCGTCAC 420
 Db 361 AGAACCTGGGCTCTCTGAAAGCATGACCGAATCTGAAACGGCTCTCGTCAC 420
 Qy 421 ACTCCCTATAACAGACACCCGCGACAACACGCGTACGGCCCTACGACAG 480
 Db 421 ACTCCCTATAACAGACACCCGCGACAACACGCGTACGGCCCTACGACAG 480
 Qy 481 CCCAGCTCACCTCTGATGCCATCCCTCAGTCAAGCATGCCACCTAC 540
 Db 481 CCCAGCTCACCTCTGATGCCATCCCTCAGTCAAGCATGCCACCTAC 540
 Qy 541 CGAGGCCGCAAGTTGACGTGCTCTCCAGCACTGAGCACCCCAAGTCGGCACC 600
 Db 541 CGAGGCCGCAAGTTGACGTGCTCTCCAGCACTGAGCACCCCAAGTCGGCACC 600
 Qy 601 TGGACGTATCCACTGAACATGAGAACTCTACTGCCAACATGCCCATC 660
 Db 601 TGGACGTATCCACTGAACATGAGAACTCTACTGCCAACATGCCCATC 660
 Qy 661 CAGATCAAGGTGATGCCACCTCTCAGGAACTCTCCATGCCCATC 720
 Db 661 CAGATCAAGGTGATGCCACCTCTCAGGAACTCTCCATGCCCATC 720
 Qy 721 AAAAAGCTGACCTGTCAGGAGGTCAGCTCCATGCCCATC 780
 Db 721 AAAAAGCTGACCTGTCAGGAGGTCAGCTCCATGCCCATC 780
 Qy 781 GAATTCAAGGAGCAAGATGCCCTCTACTGAGTAACTTGTGAAACTTCAGGGTGTGCCACCT 60
 Db 781 GAATTCAAGGAGCAAGATGCCCTCTACTGAGTAACTTGTGAAACTTCAGGGTGTGCCACCT 60

Db 781 GAATTCAACGGGGACAGATGCCCTCTAGTCATTGATTGAGTAGGGAAACAGC 840
 Qy 841 CATGCCCACTATGTAAGAGATCCCATCACAGGAAGACAGACTGTCGTTACCTATGAG 900
 Db 841 CATGCCCACTATGTAAGAGATCCCATCACAGGAAGACAGACTGTCGTTACCTATGAG 900
 Qy 901 CCACCCCAGGGTGGACTGATTCAAGACAGTCCTGACATTTCATGTTAACAGCAGT 960
 Db 901 CCACCCCAGGGTGGACTGATTCAAGACAGTCCTGACATTTCATGTTAACAGCAGT 960
 Qy 961 TGTGTTGGAGGGATAACCCCGTCAATTAAATCATGTTACCTCTGGAAACCCAGAT 1020
 Db 961 TGTGTTGGAGGGATAACCCCGTCAATTAAATCATGTTACCTCTGGAAACCCAGAT 1020
 Qy 1021 GGGCAAGTCTGGGGGACGCTGCTTGAAGCCCGGATCTGCTGCTGCCAGGAAGAC 1080
 Db 1021 GGGCAAGTCTGGGGGACGCTGCTTGAAGCCCGGATCTGCTGCTGCCAGGAAGAC 1080
 Qy 1081 AGGAAGCCGATGAAATGAGTCAGAAAGCAGCAAGTCAAAAGAACGGT 1140
 Db 1081 AGGAAGCCGATGAAATGAGTCAGAAAGCAGCAAGTCAAAAGAACGGT 1140
 Qy 1141 GATGGTACAGAAGGCCCGTTTCGTOAGAACACATGGTATCCAGATGACATCCATCAAG 1200
 Db 1141 GATGGTACAGAAGGCCCGTTTCGTOAGAACACATGGTATCCAGATGACATCCATCAAG 1200
 Qy 1201 AAACGAGAATCCCGAGATGAACTTCAGTAACTTACGTTACAGTGGCCCGTGAAGCTT 1260
 Db 1201 AAACGAGAATCCCGAGATGAACTTCAGTAACTTACGTTACAGTGGCCCGTGAAGCTT 1260
 Qy 1261 GAAATGCTGTGAAAGTCAAGACTCCCTGGAACTCATGCACTGCACTTCCCTCAGCACACA 1320
 Db 1261 GAAATGCTGTGAAAGTCAAGACTCCCTGGAACTCATGCACTGCACTTCCCTCAGCACACA 1320
 Qy 1321 ATTGAAACGTTACAGGCAACAGCAADAGCAGCAGCCAGGACTTACTTCAGAAACA 1376
 Db 1321 ATTGAAACGTTACAGGCAACAGCAADAGCAGCAGCCAGGACTTACTTCAGAAACA 1376
 SEQ ID NO: 332
 LENGTH: 2270
 TYPE: DNA
 ORGANISM: Homo sapiens

RESULT 9
 US-09-606-421B-332
 ; Sequence 332, Application US/09/606421B
 ; Patent No. 6531315
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Tongtong
 ; APPLICANT: Fan, Liqun
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Bangur, Chaitanya S.
 ; APPLICANT: Hosien, Nancy
 ; APPLICANT: Ranger, Gary R.
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Ajun
 ; APPLICANT: Skeikly, Yasir A.W.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; FILE REFERENCE: 210121.455C9
 ; CURRENT APPLICATION NUMBER: US/09/606,421B
 ; CURRENT FILING DATE: 2000-06-28
 ; NUMBER OF SEQ ID NOS: 358
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 332
 ; LENGTH: 2270
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-606-421B-332
 Query Match 48.9%; Score 1376; DB 4; Length 2270;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1376; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 61 ACAGTACTGCCCTGACCCATTACATCCAGGTTTCGAGAACCCAGCTATTTCCTCG 120
 Db 61 ACAGTACTGCCCTGACCCATTACATCCAGGTTTCGAGAACCCAGCTATTTCCTCG 120
 Qy 121 AAAGAAAGTTATTACCGATCCACATGCCAGATGAAATTCTCACT 180
 Db 121 AAAGAAAGTTATTACCGATCCACATGCCAGATGAAATTCTCACT 180
 Qy 181 CCAGAGCTTTCAGCATACTGGATTCTGGAAAGCCTATATGTCAGTTCAGCC 240
 Db 181 CCAGAGCTTTCAGCATACTGGATTCTGGAAAGCCTATATGTCAGTTCAGCC 240
 Qy 241 ATTGACTTGAACTTGTGGTGAACATCAGAAGATGGAGT 300
 Db 241 ATTGACTTGAACTTGTGGTGAACATCAGAAGATGGAGT 300
 Qy 301 AGCATGGACTCTGATCCGATCGGACTGGACCTGGTGAACCCATGTGGCCACAGTAC 360
 Db 301 AGCATGGACTCTGATCCGATCGGACTGGTGAACCCATGTGGCCACAGTAC 360
 Qy 361 ACGAACCTGGCTCTGTGACAGCATGGACTCTGGTGAACCCATGTGGCCACAG 420
 Db 361 ACGAACCTGGCTCTGTGACAGCATGGACTCTGGTGAACCCATGTGGCCACAG 420
 Qy 421 AGTCCCTATAACAGAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 480
 Db 421 AGTCCCTATAACAGAACAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 480
 Qy 481 CCCAGCTCACCTTCGATGCTCTCTCATCCCCCTAACACCCGACTAC 540
 Db 481 CCCAGCTCACCTTCGATGCTCTCTCATCCCCCTAACACCCGACTAC 540
 Qy 541 CCAGGCCGACAGTTCGACTCTCTCATCCCCCTAACACCCGACTAC 600
 Db 541 CCAGGCCGACAGTTCGACTCTCTCATCCCCCTAACACCCGACTAC 600
 Qy 601 TGGAGTATTCCACTGAACCTGAAGAACCTACTGCCAATTGAAAGCATGCCATC 660
 Db 601 TGGAGTATTCCACTGAACCTGAAGAACCTACTGCCAATTGAAAGCATGCCATC 660
 Qy 661 CAGATCAAGGTGATGCCAACCTCTCAGGGAGCTGTATCGGCCATGCTGTAC 720
 Db 661 CAGATCAAGGTGATGCCAACCTCTCAGGGAGCTGTATCGGCCATGCTGTAC 720
 Qy 721 AAAAGACTGAGCTGAGCTGAGGTTCAAGGAGCTGAGGTTCAAGCTGAGCT 780
 Db 721 AAAAGACTGAGCTGAGGTTCAAGGAGCTGAGGTTCAAGCTGAGCT 780
 Qy 781 GAATICAACGAGGACAGATGAGCTGAGGTTCAAGGAGCTGAGGTTCAAGCT 840
 Db 781 GAATICAACGAGGACAGATGAGCTGAGGTTCAAGGAGCTGAGGTTCAAGCT 840
 Qy 841 CATGCCCACTATGTAAGAATCCCATTCAAGGAAGACASAGTGTCTGTTATGAG 900
 Db 841 CATGCCCACTATGTAAGAATCCCATTCAAGGAAGACASAGTGTCTGTTATGAG 900
 Qy 901 CCACCCCAAGTGGGACTGAGATTCAAGAAGCTGTAATTTCATGTTAACAGAGT 960
 Db 901 CCACCCCAAGTGGGACTGAGATTCAAGAAGCTGTAATTTCATGTTAACAGAGT 960
 Qy 961 TGTTGTGGGGATGAACCCGGTCAATTAACTCATGTTACTCTGAAACAGAGT 1020
 Db 961 TGTTGTGGGGATGAACCCGGTCAATTAACTCATGTTACTCTGAAACAGAGT 1020
 Qy 1021 GGGCAAGTCTGGGGCGAACCCGGTCAATTAACTCATGTTACTCTGAAACAGAGC 1080
 Db 1021 GGGCAAGTCTGGGGCGAACCCGGTCAATTAACTCATGTTACTCTGAAACAGAGC 1080
 Qy 1081 AGGAAGGGCGATGAGGATACATCGAAAGGCAAGTTCGGACAGTCAAAAGACGT 1140
 Db 1081 AGGAAGGGCGATGAGGATACATCGAAAGGCAAGTTCGGACAGTCAAAAGACGT 1140

Qy 1141 GATGGTACCAAGGCCGTTCTGAGAACACATGGTATCCAGATGACATCCATCAAG 1200
 Db 1141 GATGGTACCAAGGCCGTTCTGAGAACACATGGTATCCAGATGACATCCATCAAG 1200
 Qy 1201 AAAGCAAGATCCTGAGATGAACTGTTACCTGAGGGGTGAGACTT 1260
 Db 1201 AAAGCAAGATCCTGAGATGAACTGTTACCTGAGGGGTGAGACTT 1260
 Qy 1261 GAATGCTTGTGAAAGATCAAAGACTCCCTGGAAACTCATCCAGTCAGCACACA 1320
 Db 1261 GAATGCTTGTGAAAGATCAAAGACTCCCTGGAAACTCATCCAGTCAGCACACA 1320
 Qy 1321 ATTGAAAGTACGGAAACGGAAACAGGAGCAACCAGCACTTCAAGAACAA 1376
 Db 1321 ATTGAAAGTACGGAAACGGAAACAGGAGCAACCAGCACTTCAAGAACAA 1376

RESULT 10
 US-09-630-940B-332 ; Sequence ID: 332 ; Application US/09630940B
 ; Patent No. 6737514
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Tongtong
 ; Fari, Liqun
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Bangur, Chaitanya S.
 ; APPLICANT: Hosken, Nancy
 ; APPLICANT: Panger, Gary R.
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Ajun
 ; APPLICANT: Sheiky, Yasir A.W.
 ; APPLICANT: Henderon, Robert A.
 ; APPLICANT: McNeil, Patricia D.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
 ; FILE REFERENCE: 210121-455C10
 ; CURRENT APPLICATION NUMBER: US/09/630,940B
 ; CURRENT FILING DATE: 2000-08-02
 ; NUMBER OF SEQ ID NOS: 367
 ; SOFTWARE: Fast-SEQ for Windows Version 3.0
 ; SEQ ID NO: 332
 ; LENGTH: 2270
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-630-940B-332

Query Match 48.9%; Score 1376; DB: 4; Length 2270;
 Best Local Similarity 100.0%; Pred. No. 0;
 Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTGTATCAAAGACAGTGTGGAAATTTGAAACACTACCGTTGTGCACCCCT 60
 Db 1 TCGTGTATCAAAGACAGTGTGGAAATTTGAAACACTACCGTTGTGCACCCCT 60
 Qy 61 ACACTCTGCCCTGACCCCTACATCAGGGTTTCATGCAATTTCTTCTTGG 120
 Db 61 ACACTCTGCCCTGACCCCTACATCAGGGTTTCATGCAATTTCTTCTTGG 120
 Qy 121 AAAGAAAGTTATTACCGATCCCATGTCAGGACACAGAACATGAAATTCTCAGT 180
 Db 121 AAAGAAAGTTATTACCGATCCCATGTCAGGACACAGAACATGAAATTCTCAGT 180
 Qy 181 CCAGGGTTTCCAGCATTCGGATTCAGCTGCTATGCTTCAGGCTATGCTTCAGC 240
 Db 181 CCAGGGTTTCCAGCATTCGGATTCAGCTGCTATGCTTCAGGCTATGCTTCAGC 240
 Qy 241 ATTGACTGAACTTGTGGATGACATGAAAGATGTTGCAAGATGAGTT 300
 Db 241 ATTGACTGAACTTGTGGATGACATGAAAGATGTTGCAAGATGAGTT 300

Qy 301 AGCATGGACTGTATCCGATGCAAGGACTGGGACCTGGACAGTCAAGAGCT 360
 Db 301 AGCATGGACTGTATCCGATGCAAGGACTGGGACCTGGACAGTCAAGAGCT 360

i TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
 i FILE REFERENCE: 201021-555C11
 i CURRENT APPLICATION NUMBER: US/09/643 ,597
 i CURRENT FILING DATE: 2000-08-21
 i NUMBER OF SEQ ID NOS: 369
 i SOFTWARE: Fast-SEQ for Windows Version 3.0
 i SEQ ID NO: 337
 i LENGTH: 1551
 i TYPE: DNA
 i ORGANISM: Homo sapiens
 US-09-643-557-337

Query Match	43.8%	Score 1232; DB 3; Length 1551;	Db	841 CCRATTAAATCTGTAACAGGATGGCAACTGGCCAGCTGC 900
Best Local Similarity	100.0%	Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;	Qy	1045 TTGAGGCCGATCTGCTTGTGAAAGAAGACGGAAAGCTGATAGCATC 1104
Matches 1232: Conservative	0;		Db	901 TTGAGGCCGATCTGCTTGTGAAAGAAGACGGAAAGCTGATAGCATC 960
Qy	145 ATGTCGGACAGCACACAATGAAATTCTCTAGTCAGGAGTTTCAGATACTGG 204	Db	9105 AGAAAGAGCAAGTTGGACAGTCAAAGAACGTTGATGGTACGAAGGCCGTTTGT 1164	
Db	1 ATGTCGGACAGCACACAATGAAATTCTCTAGTCAGGAGTTTCAGATACTGG 60	Qy	961 AGAAAGAGCAAGTTGGACAGTCAAAGAACGTTGATGGTACGAAGGCCGTTTGT 1020	
Qy	205 GATTTCCTGAAACAGCCTATATGTTCAAGTCCATTGAACTTGTTGAA 264	Db	1165 CAGAACACACATGGTATCCAGATCATCCATCAAGAACGAGATCCCAGATGATGAA 1224	
Db	61 GATTTCCTGAAACGCTATATGTTCAAGTCCATTGAACTTGTTGAA 120	Db	1021 CAGAACACACATGGTATCCATCAAGAACGAGATCCCAGATGATGAA 1080	
Qy	265 CCATCAGAGATGTTGCCAACAAAGATTGAGATTACATGGACTGTATCGGCATGCAAG 324	Qy	1165 CAGAACACACATGGTATCCAGATCATCCATCAAGAACGAGATCCCAGATGATGAA 1224	
Db	121 CCATCAGAGATGTTGCCAACAAAGTTGAGATTACATGGACTGTATCGGCATGCAAG 180	Db	1225 CTGTATACTTACCACTGAGGGCCCTGAGACTTATGAAATCTGTTGAAAGTCAAAGAG 1284	
Qy	325 GACTGGGACTGTGAACTGACGGCCATGTGGCACAGTACAGGAACCTGGGCTCTGAAAGC 384	Db	1081 CTGTATACTTACCACTGAGGGCCCTGAGACTTATGAAATCTGTTGAAAGTCAAAGAG 1140	
Db	181 GACTGGGACTGTGAACTGACGGCCATGTGGCACAGTACAGGAACCTGGGCTCTGAAAGC 240	Qy	1285 TCCCTGAAACTCATGCACTTCTCAGCACATTGAAACCATTTGAAACACTGAAAGCAA 1344	
Qy	385 ATGGACCCAGCAAGTTCAAGAACGGCTCTGTCCACCAAGTCCCTATAACACGACCACCG 444	Db	1141 TCCCTGAAACTCATGCACTTCTCAGCACACATTGAAACACTGAAAGCAA 1200	
Db	241 ATGGACCCAGCAAGTTCAAGAACGGCTCTGTCCACCAAGTACAGAACCCCTCTGAAAGC 300	Qy	1345 CAGCAGCAGCAGGACACTTACTTCAGAACAA 1376	
Qy	445 CAGAACACGGTCACGGGCCCTCGCCCTAACGGCAACGGCAGCTCCATGTCATGCTCTC 504	Db	1201 CAGCAGCAGCAGGACACTTACTTCAGAACAA 1232	
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Search completed: October 3, 2005, 09:27:59
 Job time : 459 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_p2n mode!

Run on: October 3, 2005, 06:01:58 ; Search time 936 Seconds
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Title: US-09-670-568C-1

Perfect score: 2383

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Scoring table: BLOSUM62
 Xgapop 10.0 , Xgapext 0.5
 Ygapop 10.0 , Ygapext 0.5
 Fgapop 6.0 , Fgapext 7.0
 DelOp 6.0 , DelExt 7.0

Searched: 7445561 seqs, 3452328358 residues

Total number of hits satisfying chosen parameters: 14885122

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
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2	2383 100.0	2816	9	US-09-735-05-373
3	2383 100.0	2816	9	US-09-850-716A-33
4	2383 100.0	2816	9	US-09-897-778-333
5	2383 100.0	2816	14	US-10-007-700-333
6	2383 100.0	2816	15	US-10-117-922-333
7	2383 100.0	2816	16	US-10-393-590-36
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18	2383 100.0	2816	16	US-10-313-986-333
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ALIGNMENTS

RESULT 1
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 Sequence 3, Application US10716359
 Publication No. US20040132120A1
 GENERAL INFORMATION:
 APPLICANT: Yang, Annie
 INVENTION: Cell Regulatory Genes, Encoded Products, And Uses
 RELATED THERETO
 CURRENT APPLICATION NUMBER: US10/716,359
 CURRENT FILING DATE: 2003-11-18
 PRIOR APPLICATION NUMBER: US-09/174,493
 PRIOR FILING DATE: 1998-10-15
 PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/087,219
 PRIOR FILING DATE: EARLIER FILING DATE: 1998-05-29

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/062,076
 PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-15
 NUMBER OF SEQ ID NOS: 50
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 3
 LENGTH: 1347
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(1344)
 JS-10-716-359-3

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; Patent No. US20020052329A1			
; GENERAL INFORMATION:			
; APPLICANT: Wang, Tongtong			
; APPLICANT: Fan, Liqun			
; APPLICANT: Kalos, Michael D.			
; APPLICANT: Bangur, Chaitanya S.			
; APPLICANT: Hosken, Nancy			
; APPLICANT: Fanger, Gary R.			
; APPLICANT: Li, Samuel X.			
; APPLICANT: Wang, Aijun			
; APPLICANT: Skeiky, Yasir A.W.			
; APPLICANT: Henderson, Robert A.			
; APPLICANT: McNeill, Patricia D.			
; APPLICANT: Fanger, Neil			
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY			
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER			
; FILE REFERENCE: 210121-455C14			
; CURRENT APPLICATION NUMBER: US/09/735,705			
; NUMBER OF SEQ ID NOS: 419			
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; SEQ ID NO 333			
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; ORGANISM: Homo sapiens			
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685	CCTCAGGGAGCTGTTATCGCCCAATGCCATGCTGCTACAAGCTGAGCACTCAAGGAG	744				
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221	ProProSerHisLeuIleArgValGluGlyAsnSerSerHisAlaGlnItyrValGluAspPro	240				
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925	ACGACAGTCCTGTCATAATTCTATGTGTAAACCACTGTTGGAGGTGACCCCCGT	984				
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1285	TCCCTGGAAACCTCATGAGTACCTCTCCATGACACATGAAACAGCAACAGCAA	1344				
401	GinGlnIlnHiisGlnHiisLeuLeuGlySerAspGlySerAspValPhePheArgHiisSerLys	440				
1345	CAGGAGCAGACCAGCACTTACTTCGAAACATCTCCCTCAGCAACAGCAA	1464				
421	IleValGluProArgGluThrProLysGlnSerAspValPhePheArgHiisSerLys	440				
1405	CTTGTGTGAGCCGGGAGAGAAACTGAGCTGAGCTCTCTTAACTGAGTCTGAGTCAAG	1464				
565	TCTCCATCACCGCCATCCCCCTCCAAACACGGACTTCCGCTTACGCAAGCTTCAACGTC	564				
141	SerPheGlnGlnSerSerThrAlaLysSerAlaThrPheAspPheAspVal	140				
505	TCTCCATCACCGCCATCCCCCTCCAAACACGGACTTCCGCTTACGCAAGCTTCAACGTC	564				
624	CTCTTCAGCAAGTGGCAACTGAGTCTCTTAACTGAGTCTGAGTCAAG	624				

161 LysLeutArgCysGlnIleAlaLysThrCysProLeuGlnLysLeuValMetThrPro 180
 162 Rett, Marc W.
 625 Durham, Margaret A.
 ; APPLICANT: Panger, Gary R.
 ; APPLICANT: Vedrick, Thomas S.
 ; APPLICANT: Carter, Derrick
 ; APPLICANT: Watanabe, Yoshihiro
 ; APPLICANT: Peckman, David W.
 ; APPLICANT: Cai, Feng
 ; APPLICANT: POY, Tessa M.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; OF CANCER AND DIAGNOSIS OF LONG CANCER
 ; FILE REFERENCE: 210121-455C17
 ; CURRENT APPLICATION NUMBER: US10/007,700
 ; CURRENT FILING DATE: 2001-11-30
 ; NUMBER OF SEQ ID NOS: 469
 ; SOFTWARE: FastSTO for Windows Version 4.0
 ; SEQ ID NO: 333
 ; LENGTH: 2816
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-007-700-333

Alignment Scores:
 Pred. No : 1.21e-276 Length: 2816
 Score: 238.00 Matches: 448
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 14

US-09-670-568C-1 (1-448) × US-10-007-700-333 (1-2816)

281 ProfileLeuLeileValThrLeuGluThrArgAspGlyCinvalLeuGlyArgArgCys 300
 985 CCAATTAACTATGGTACTCTGGAACAGATGGGAACCCATGCCAGATGATCCC 1044
 261 ThrThrValLeuTyrrAsnPhiMetCysAsnSerSerCysValGlyMetAsnArgArg 280
 865 ATCACGGAGACAGACAGTGCTGACTTGTGCAATGATTC 924

282 AspAspGlyAlaLeuGluLeuAsnPhiValAspLeuAsnPhiValAspGlu 281
 925 ACGAGACTGTGTACAATTCTATGGTAACGACTTGTGTTGGGGTGAACGGCCST 984

283 GlnAsnGlnSerThrGlnThrAspGluLeuSerProGluValPheGlnHisIleTrp 20
 1105 AGAACGGAGGTTTCGAGCAGTACAAAGAACGCTTCATGGCTTCCAGGGCATCTGG 1164

284 GlnAsnGlnSerThrGlnMetThrSerIleLysLysArgArgSerProAspGlu 360
 1165 CAGAAACACATGGTATCAGATGACATCCATCAAAGAAGATCCCAAGATGATA 1224

285 LeuLeuTyrrLeuProValArgGlyArgGlyThrIleGluMetLeuLeuLysIleLysGlu 380
 1225 CTGTGTATACCTTACCGTAGGCCGCTGAGACTTATGAATGCTGAGATCAAAGGG 1284

286 SerLeuGluLeuMetGlnIleValProGlnHisthrIleGluLysIleGluLeuGlyArgGlnGln 400
 1285 TCCCTGGAACTCATCGAACCTCTCCTCACACGACAACTCCAGCAACAGGCA 1344

287 GlnGlnGlnHisGlnHisIleLeuLeuSerAlaCysPheArgAsnGlu 420
 1345 CAGCAGCAGACCACACTACTTGAACATCCTTCAGCTGCTCAGGAATGG 1404

288 LysValGlyProIleGlyGluThrProLysGlnSerAspValPhePheArgHisSerLys 440
 1405 CTTGTTGGAGCCCCGGAGAGAAACTCCAACAAATCTGAATCTCTTGTAGATCCAG 1464

289 ProProAsnArgSerValtyrrPro 448
 1465 CCCCCAACCGATCAGTGTACCA 1488

RESULT 5
 US-10-007-700-333
 ; Sequence 333. Application US/10007700
 ; Publication No. US2003064947A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Tongtong
 ; APPLICANT: Wang, Ajun
 ; APPLICANT: Skeky, Yasir A.W.
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Cai, Feng
 ; APPLICANT: POY, Tessa M.
 ; APPLICANT: Peckman, David W.
 ; APPLICANT: Vedrick, Thomas S.
 ; APPLICANT: Carter, Derrick
 ; APPLICANT: Watanabe, Yoshihiro
 ; APPLICANT: Cai, Feng
 ; APPLICANT: Rett, Marc W.
 ; APPLICANT: Durham, Margaret A.
 ; APPLICANT: Panger, Gary R.
 ; APPLICANT: Vedrick, Thomas S.
 ; APPLICANT: Carter, Derrick
 ; APPLICANT: Watanabe, Yoshihiro
 ; APPLICANT: Peckman, David W.
 ; APPLICANT: Cai, Feng
 ; APPLICANT: POY, Tessa M.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; OF CANCER AND DIAGNOSIS OF LONG CANCER
 ; FILE REFERENCE: 210121-455C17
 ; CURRENT APPLICATION NUMBER: US10/007,700
 ; CURRENT FILING DATE: 2001-11-30
 ; NUMBER OF SEQ ID NOS: 469
 ; SOFTWARE: FastSTO for Windows Version 4.0
 ; SEQ ID NO: 333
 ; LENGTH: 2816
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-007-700-333

Alignment Scores:
 Pred. No : 1.21e-276 Length: 2816
 Score: 238.00 Matches: 448
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 14

US-09-670-568C-1 (1-448) × US-10-007-700-333 (1-2816)

281 AspAspGlyAlaLeuGluLeuAsnPhiValAspLeuAsnPhiValAspGlu 281
 145 ATGTCGACGGCATAAGACACATTCCTCAGTCCAGGGTTTCCAGGCATCTGG 204

282 AspAspGlyAlaLeuGluGlnProLysCysSerValGlnProLysAspLeuAsnPhiValAspGlu 40
 205 GATTTCCTGGAACACGCCATATGTCAGTCCAGCCATGACTGAACCTTGATGAA 264

283 ProSerGluAspGlyAlaLeuThrAsnLysIleGluLysSerMetAspCysIleArgMetGln 60
 265 CCATCGAGATGGTGCAGAAAAGATGAGATTAGCATGGATCTGATCGCTGAGCAG 324

284 AspSerAspLeuSerAspPromoterProGlnGlyThrAsnLeuGlyLeuLeuSer 80
 325 GACCTGGACCTGAGTCGCCATGGGCCACAGTACGACGAACTGGGCTCTGACAGC 384

285 MetAspGlnIleGlnAsnGlySerSerSerSerProTyrrAsnThrAspIleAla 81
 385 ATGGACAGGAGATCAGACGGCTCTGTCCACAGCAGACCCATTAACACAGACCGCG 444

286 GluAsnSerValIleProSerProTyrrAlaGlnProSerSerThrAspAlaLeu 120
 445 CAGAACAGCCTCACGGCCCTCCACCTAGCAGCCACGCTCTGATGCTCTC 504

287 SerProSerProAlaIleProSerProTyrrAlaGlnProSerSerThrAspAlaLeu 121
 505 TCCTCATACCCGCACTCCCTCACACGCTCAGCCACGCTCTGATGCTCTC 564

288 SerPheGlnSerSerThrAlaIleAlaLysSerAlaThrTrpThrTyrsSerThrGluLeuLys 160
 565 TCCCTCAGAGTCAGCCACGCTGCACTGAGTCAAGTCAGCTGAACTGAACTGAA 624

289 LysLeuGlyCysGlnIleLeuAlaLysSerThrCysProLysCysProLysCys 161
 625 AAACCTACTGCCAAATTGCCAAAGACATGCCCATCCAGTCAGTCAAGCTGATGAC 684

290 ProGlnGlyAlaValIleArgAlaMetProValtyrrLysLysAlaGluLysValThrGlu 200
 181 ProGlnGlyAlaValIleArgAlaMetProValtyrrLysLysAlaGluLysValThrGlu 200

291 CCTCTGGGAGCTGTTATGCCGCATGCCCTACGCTGCTGCTCAGCTGGAG 744
 685 CCTCTGGGAGCTGTTATGCCGCATGCCCTACGCTGCTGCTCAGCTGGAG 744

QY	401	GlnGlnGlnHisGlnHistLeuGlnLysHisIleLeuSerAlaCysPheArgAsnGlu	420	Db	565	TCTTCCAGAGTCGAGACGCCACTCTGGCCACTCTGGATTTACTGAACTGAAAG	624
	1345	CAGAGCACACCGCACTACTCTAGAACACTCTCTTCAGGATGAAATGAG	1404	QY	161	LysLeuTyrCysGlnIleAlaLysThrCysProIleGlnIleValMetThrProPro	180
Db	625	AACTCTACTGCCAAATTGCAAAAGACATGCCCATCCAGATCAAGGTGATGACCCACCT	684	Db	181	ProGlnGlyAlaValIleArgGalaMetProValtryLysAlaGlnIleValThrGlu	200
DY	421	LeuValGluProArgArgGluThrProlysGlnSerAspValPhePheArgHisSerIys	440	QY	685	CCCTAGGGAGCTGTTATCGCGCATGCTTGCTACAAAAAAACTGAGCACCGTCA CGGAG	744
Db	1405	CTTCGGACCCCGAGAACAACTCCAAACAACTCTGAGCTCTCTAGACATTCCAG	1464	Db	201	ValValIlysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla	220
DY	441	ProProAspArgSerValTyrPro	448	QY	745	GtGTTGAGCGGTGCCAACATGAGTGAAGGACAGATGTCAGGGACAGATGCC	804
Db	1465	CCCCCDBAACCGATCTGTGACCCA	1488	Db	221	ProProSerHisIleArgValGluGlyAsnSerHisAlaGlnItyValGluAspPro	240
QY		Sequence 27, Application US/10393590		Db	805	CCCTCCTACTCATTGATTGAGTCGAGTAGGGAAACAGCCATGCCCAGTATGAGATCCC	864
GENERAL INFORMATION:		Publication No. US20030190656A1		QY	241	IleThrGlyArgGlnSerValLeuValProGlnValGlyIleGluGly	260
APPLICANT: WANG, YIXIN		FILE OF INVENTION: BREAST CANCER PROGNOSTIC PORTFOLIO		Db	865	ATCACGAAAGACAGAGTGTGACTGACTGAACTGAACTGAACTGAACTGAACTC	924
CURRENT APPLICATION NUMBER: US/10/393,590		CURRENT FILING DATE: 2003-03-21		QY	261	ThrThrValLeuTyroAsnPheMetCysAsnSerCysValGlyMetAsnArgArg	280
PRIOR APPLICATION NUMBER: 60/368,789		PRIOR FILING DATE: 2002-03-29		Db	925	ACCACAGITGTAATTCTGACATTGTTACAGAGTGTGAGGGATGAAAGCCCGT	984
NUMBER OF SEQ ID NOS: 100		SEQUENCE ID NO: 27		QY	281	ProIleLeuIleValThrLeuGluThrArgAspGlyGlnValLeuGlyArgArgCys	300
SOFTWARE: PatentIn version 3.1		LENGTH: 2816		Db	985	CCAAATTCTTAATCTGTTACTCTGGAAACCTGAGATGGCAAACTCTGGCGAGCTGC	1044
TYPE: DNA		ORGANISM: human		QY	301	PhoGluAlaArgIleCysAlaCysProGlyArgAspArgLysAlaAspGluAspSerIle	320
SEQ ID NO: 10-393-590-27		Db	1045	TTTGAGGCCGGATCTGTGCTTGGCCAGGAAGGGATGAAAGATAAGCATC	1104		
Alignment Scores:		Length: 2816		QY	321	ArgLYsGlnGlnValSerAspSerThrIlysAsnGlyAspGlyThrLyArgProPheArg	340
Query seqd. No.: 1		Matches: 2813		QY	325	ArgLYsGlnGlnValSerAspSerThrIlysAsnGlyAspGlyThrLyArgProPheArg	340
Score: 283.00		Percent Conservative: 100.00%		Db	1105	AGAAAGCGACAAGTTGACAGTCAAAGAACGGTGTGAGGAAAGGCCCTTGTG	1164
Percent Similarity: 100.00%		Mismatches: 0		Db	1225	CTGTTTACTTACCGAGGGCCGTGAGACTTGTGAATGCTGTTGAGAATCAARGAA	1284
Best Local Similarity: 100.00%		Indels: 0		QY	341	GlnAsnThrHisGlyIleGlnMetThrSerIleIlysArgArgSerProAspAspGlu	360
Query Match: 16		Gaps: 0		Db	1165	CAGAACACACATGATGACATGACATCCATCAAGAACGAACTCCAGATGATGAA	1224
US-09-670-568C-1 (1-448) × US-10-393-590-27 (1-2816)		QY	361	LeuLeuTyrLeuProValArgGlyArgGluThrTyrGluMetLeuLeuIleIlysGlu	380		
DY	1	MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTrp	20	Db	1225	CTGTTTACTTACCGAGGGCCGTGAGACTTGTGAATGCTGTTGAGAATCAARGAA	1284
Db	145	ATGTCACAGCAAGCACAGCAAAATGAATTCCTCAGTCAGTCAGCTATCTGG	204	QY	381	SerLeuGluLeuMetGlnItyIleProGlnHisThrIleGluThrTyrArgGlnGln	400
DY	21	AspPheLeuGlnProIleGlnProIleAspLeuAspPheValAspGlu	40	Db	1285	TCCCTGGAACTCATGCAACTTCTCAGAACATCTCCAGAACATCTCCAGAACAT	1344
Db	205	GATTTTCGAAACAGCCPATATGTTCAAGTCAGTCAGCTGACTCTGAA	264	QY	401	GlnGlnGlnHisGlnHisLeuLeuGlnIlyShiSleLeuLeuSerAlaCysPheArgAsnGlu	420
DY	41	ProSerGluAspGlyAlaIleThrAsnLysIleGluIleSerMetAspCysBilearGlyMetGln	60	Db	1345	CAGCAGCAGCACCAGCACCCTTCAGAACATCTCCAGAACATCTCCAGAACAT	1404
Db	265	CCATCAGAGATGTCGCAAAACAGATGAGATTGAGATTGAGCTGACTCTGAA	324	QY	421	LeuValGluProArgArgGluThrProlysGlnSerAspValPhePheArgHisSerIys	440
DY	61	AspSerAspLeuSerAspProMetTrpProGlnItyThrAsnLeuGlyLeuLeuAsnSer	80	Db	1405	CTTGTGGAGCCGGAGAACACTCAAAACATCTGAGCTCTTGTAGACATTCCAAAG	1464
Db	325	GACTCGGACCTGACTGACCCCCATGGCCACAGTACACCAACTCTGGCCCTCTGAAACAGC	384	QY	441	ProProAsnArgSerValTyrPro	448
DY	81	MetAspGlnGlnIleGlnAsnGlySerSerSerSerIleProTyrAspThrAspHisAla	100	Db	1465	CCCCAAAACCGATCAGTGTACCCA	1488
Db	385	ATGGACCAAGAGATTCAAGACGGCTTCTGGCCCTCCAGCCATGACCCG	444	RESULT 9			
DY	101	GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerSerThrPheAspAla	120	US-10-393-590-64			
Db	445	CAGACAGGGTCAGGGCCCTCCCTCAAGCCAGTCGACAGCCAGTCGCTTC	504	; Sequence 64, Application US/10393590			
DY	121	SerProSepProAlaIleProSerAsnThrAspTyrProGlyProHisSerPheAspVa	140	; GENERAL INFORMATION:			
Db	505	TCTTCATCAGCCCATCCCTCCAAACGACTTACAGGGCCGACAGTCGACTT	564	; APPLICANT: WANG, YIXIN			
DY		SetPheGlnGlnSerSerThrAlaIleArgSerAlaIleLeuIle		; TITLE OF INVENTION: BREAST CANCER PROGNOSTIC PORTFOLIO			
DY				; FILE REFERENCE: CDS 268 US NP			
DY				; CURRENT APPLICATION NUMBER: US/10/393,590			
DY				; PRIORITY APPLICATION NUMBER: 2003-03-21			
DY				; CURRENT FILING DATE: 2003-03-21			

PRIOR FILING DATE: 2002-03-29
 NUMBER OF SEQ ID NOS: 100
 SOFTWARE: Patentin version 3.1
 SEQ ID NO 64
 LENGTH: 2816
 TYPE: DNA
 ORGANISM: human
 US-10-393-590-64

Alignment Scores:
 Pred. No.: 1.21e-276 Length: 2816
 Score: 2383.00 Matches: 448
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00%
 Query Match: 100.00%
 DB: 16 Gaps: 0

US-09-670-568C-1 (1-448) x US-10-393-590-64 (1-2816)

Qy 1 MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGlnHisIleTrp 20
 Db 145 ATGTCAGACAGAACACAGAACAAATGAAATTCTCAGTCCAGGGTTTCAGCATATCTGG 204
 Qy 21 AspPheLeuGluGlnProIleCysSerValGlnProIleAsnLeuAsnLeuAspGlu 40
 Db 205 GATTTCGGACAGCTATATGTTCAGCCATTGTAACCTTGATGAA 264
 Qy 41 ProSerGluAspGlyAlaThrAsnLysIleSerIleAspCysIleArgMetGln 60
 Db 265 CCATCGAAGATGGTGCAGACAAAGATTAGATTAGCATGGACTGTACCGATGAG 324
 Qy 61 AspSerAspLeuSerAspProMetTrpProGlnTyrrhrasLeuGlyLeuAsnSer 80
 Db 325 GACTGGACCTGAGTCACCCATGTGCCAGTACAGAACCTGGCCCTCTGTGAAACSC 384
 Qy 81 MetAspPheGlnIleGlnAsnGlySerSerSerSerSerSerProTyroAsnThrAspHisIleAla 100
 Db 385 ATGGACCAGGAGATTAGAACGGCTCCTGTCCACCGTCCCTATAACAGACCAACCG 444
 RESULT 1.0
 US-10-393-590-65
 Sequence 65 , Application US/10393590
 Publication No. US20030190656A1
 GENERAL INFORMATION:
 APPLICANT: WANG, YIXIN
 TITLE OF INVENTION: BREAST CANCER PROGNOSTIC PORTFOLIO
 FILE REFERENCE: CDS 268 US NP
 CURRENT APPLICATION NUMBER: US/10/393,590
 CURRENT FILING DATE: 2003-03-21
 PRIOR APPLICATION NUMBER: 60/368,789
 PRIOR FILING DATE: 2002-03-29
 NUMBER OF SEQ ID NOS: 100
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 65
 LENGTH: 2816
 TYPE: DNA
 ORGANISM: human
 US-10-393-590-65

Alignment Scores:
 Pred. No.: 1.21e-276 Length: 2816
 Score: 2383.00 Matches: 448
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 100.00% Indels: 0
 Query Match: 16 Gaps: 0

US-09-670-568C-1 (1-448) x US-10-393-590-65 (1-2816)

Qy 1 MetSerGluSerThrGlnThrAsnGluLeuSerProGluValPheGlnHisIleTrp 20
 Db 865 ATCACGGAAAGACAGGTGTCCTGTTGACCTTAGGCCACCGTGAATTC 924
 Qy 261 ThrThrValLeuTyroAsnPhenMetCysAsnSerSerCysValGlyMetAspArg 280

Qy 241 IleThrGlyArgGlnSerValLeuValProProGluValGlyThrCluPhe 260
 Db 805 CCTCCCTAGTCAATTGATTGAGTACGGGACAGCCAGATGAGATGCC 864
 Qy 865 ATGTCAGGACAGCAACCATGAGCTAACGTTCAACGGGACAGATGCC 924
 Qy 21 AspPheLeuGluGlnProIleCysSerValGlnProIleAsnPheValAspGlu 40

Db	1285	TCCCTGAACTCATGAGTACCTTCTAGCACACATTGAAACGTACAGCAA 1344	Qy	141	SerPheGlnGlnSerSerThrAlaLysSerAlaThrPheThrTyrSerThrGluLeuLys 160
Qy	401	GlnGlnGlnHisGlnHistLeuLeuLysIleSerAlaCysPheArgAsnGlu 420	Db	565	TCCCTCCAGAAGTCAGGCCAACGCGCAAGTGCGCTCCACTGAACTGAA 624
Db	1345	CAGCGCAGACCCAGCACTTCAAGAACATCTCTTCAGGATGAG 1404	Qy	161	LysLeuTyrCysGlnIleAlaLysThrCysProleGlnIleLysValMetThrProPro 180
Qy	421	LeuValGlnProArgArgGluThrProLyGlnSerAlaPhePheAlaGlnSerLys 440	Db	625	AAACTCTACTGCCAAATGCCAACATGCCCATCCAGATCAGTGTGATGCCACCT 684
Db	1405	CTTGTCGAGGCCGGAGAAGAACTCCAAAACAATCTGACSTCTTTAGACATTCAG 1464	Qy	181	ProGlnGlyAlaValIleLeuGlnAlaMetProValTyrLysAlaGluHisValThrGlu 200
Qy	441	ProProAsnArgSerValArgSerValArgSerValArgSerValArg 448	Db	685	CCTCAGGGAGCTGTTATCGGCATGCCCAGTCACGGTACGGAG 744
Db	1465	CCCCCAACCGATCATGTAACCA 1488	Qy	201	valValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyLleAla 220
Db	745	GTGNGAAAGGGTCCCCAACATGAGCTGAGCCGATTCAAGGGCACAGTTGCC 804	Qy	221	ProProSerHisIleIleLeuIleArgValGluGlyIleAsnSerHisIleAlaGlnTYrValGluAspPro 240
Db	805	CCTCTAGTCATTCGATGAGTAGGGGAACAGGCCATGCCAGTATGTAAGATCCC 864	Qy	241	IleThrGlyArgGlnSerValLeuValProTyrsLipProProGinValGlyThreIlePhe 260
Db	865	ATCAAGGAGACAGAGTGTCTGTTACTTATGCCACCCAGTTGGACTGATTGAA 924	Qy	261	ThrThrValLeuIleThrAsnPheMetCysAsnSerCysValGlyGlyMetAsnArgArg 280
Db	925	ACGACAGCTTGPAACATTCTGTTACAGGATTGTTACAGGATTGTTACAGGATTGAA 925	Qy	281	ProIleLeuIleLeuIleValGluThrArgAspGlyGlnValLeuGlyAsnArgCys 300
Db	985	CCAATTAAATCATGTTACTCTGGAAACCAGATGGCAAACTGCTGGCCGAGCTGC 1044	Qy	301	PheGluIlaAarArgIleCysAlaCysProGlyArgAspArgLysAlaAspGluAspSerIle 320
Db	1045	TTTGAGGCCGGATCTGCTGCTGAGTCAGTACAGTAAAGAACCTCCAGATGATGAA 1104	Qy	321	ArgLysGlnGlnValSerAspSerThrIleAsnGlyAspGlyThrLysArgPheAspArg 340
Db	1105	AGAAAGCAGCAAGTTGCAAGCTCATCCATCAAAGAACATCTCCAGATGAA 1164	Qy	341	GlnAsnThrHisGlyIleGlnMetThrSerIleLysLysBargArgSerProAspAspGlu 360
Db	1165	CAGAACACACATGCTATCCAGATGACATCCATCAAAGAACATCTCCAGATGAA 1224	Qy	361	LeuLeuTyrLeuProValArgGlyArgGluThrThrGluMetIleLeuLysIleGlu 380
Qy	1	MetSerGlnSerThrGlnThrAsnCluPheLeuSerProGluAlaPheValAspGlu 20	Db	1225	CTGTATACCTACCATGAGGGCCGTGAGACTATGAAATGCTGTTGAGATCAAAGAG 1284
Db	145	ATGTCAGCAAGCACAGCAAATAATTCTCATGCTGATATCG 204	Qy	381	SerIleGluLeuMetGlnTyrLeuProGlnHisThrIleGluThrTyrArgGlnGlnGln 400
Qy	21	AspPheLeuGluGlnProIleCysSerValGlnProIleAspIleAsnPheValAspGlu 40	Db	1285	TCCCTGGAACTCATGAGTCTCAGCACAAATGAAACGTACAGGCAACAGCAA 1344
Db	205	GATTTCTGAAACGCCATTATGTTCACTGAGCTCAGGCCATGAACTTTGNGATGA 264	Qy	401	GlnGlnGlnHisGlnHisIleLeuLeuSerAlaCysPheArgAsnGlu 420
Qy	41	ProSerGluAspGlyAlaIleThrAsnLysIleGluIleSerMetAspCysS1IleArgMetGln 60	Db	1345	CAGCAAGCACCACGACTTACTTCAGAAACATCTCCITTCAGGCTCAGATGAG 1404
Db	265	CCATCAGAAATGGTGCACAAACAGTTGAGATTGGACTATCCGCATGAG 324	Qy	421	LeuValGluProArgArgGluThrProLySlnSerAspValPheArgHisSerLys 440
Qy	61	AspSerAspIleSerAspProMetTrpProGlnItyrThrAsnIleGlyIleAspSer 80	Db	1405	CTTGAGGCCAGTCAGTGGCAACAGTGGCTTCAGCTTGTGACATTCAG 1464
Db	325	GACTGGACATGAGTGAACCCATGGGCACAGTTGAGATTGGACTATCCGCATGAG 384	Qy	441	ProProAsnArgSerValTyrPro 448
Qy	81	MethPheGlnGlnIleGlnAsnGlySerSerSerSerSerSerSerSer 100	Db	1465	CCCCAAACCGATCAAGTACCA 1488
Db	385	ATGGACCAAGCAGAGTCAGGCCAGCTCAGGCCATGAGCTCAGGCCACCG 444	RESULT 15		
Qy	101	GlnAsnSerValIleAlaProSerProTyrsProIleSerThrAspAlaLeu 120	US-10-94-087-26	Sequence 26 , Application US/10394087	
Db	445	CAGACAGGGTCAAGGGCCCTGCCTCAGGCCAGCTCACCCTCGATGCTCTC 504	US-10-0301947341	Application No. US200301947341	
Qy	121	SerProSerProAlaIleProSerAsnThrAspItyrProHisSerPheAspVal 140	GENERAL INFORMATION:		
Db	505	TCTCCATCACCCGCCATCCCTCAAACACGACTACCCGGAGAAACTCTGAC 564	APPLICANT: JATKO, Tim		
		TITLE OF INVENTION: SELECTION OF MARKERS			
		FILE REFERENCE: CDS 265 US NP			
		CURRENT APPLICATION NUMBER: US/10/394 , 087			

CURRENT FILING DATE: 2003-03-21
 PRIORITY APPLICATION NUMBER: 60/368,790
 NUMBER OF SEQ ID NOS: 100
 SEQ ID NO: 26
 LENGTH: 2816
 TYPE: DNA
 ORGANISM: human
 US-10-394-087-26

Alignment Scores:

Pred No.	Length:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:
1.21e-276	2816	2383.00	100.00%	100.00%	100.00%	US-09-670-568C-1 (1-448) × US-10-394-087-26 (1-2816)
		448	0	0	0	
			Mismatches:	Indels:	Gaps:	
			0	0	0	

Qy 1 MetSerGlnSerThrGlnThrAsnGluPheIeuSerProIleUvaPheGlnHisIleTrp 20
 Db 145 ATGTCCAGAGCACACAGAACAAATGATTCAGCAATGATCG 204

Qy 21 AspPheLeuGluGlnProIleCysSerValGlnProIleAspLeuAsnPheValAspGlu 40
 Db 205 GATTTCGAAACACCTTATATGTTCACTTGACCTTCAGCCATTCTCACTCCAGGGTTTCAGCAATGATCG 264

Qy 41 ProSerGluAspGlyAlaThrAsnLysIleGluIleSerMetAspCysIleArgMetGln 60
 Db 265 CCATCGAACATGGTGCACACAGATGAGATTAGATGCTGATCCGCATGCG 324

Qy 61 AspSerAspIeuSerAspIlePromeTrpProGlnTrpThrAsnLeuGlyLeuLeuAsnSer 80
 Db 325 GACTCGAACCTGAGTGACCCATGNGCACAGAACAGATGAGATTAGATGCTGATCCGCATGACAC 384

Qy 81 MetAspGlnGlnIleGlnAsnGlySerSerSerThrSerProTyrAsnThrAspHisAla 100
 Db 385 ATGGACCAGCAGATTCAAGACGGCTCTCCACCGCTTACACGACACCGGG 444

Qy 101 GlnAsnSerValThrAlaProSerProTyrAlaGlnProSerSerThrPheAspAlaLeu 120
 Db 445 CAGAACAGCGTACAGGCCCTCGCCCTAGCCACAGCATGCCCATTGAGATGACCTTC 504

Qy 121 SerProSerProAlaIleProSerIeuSerSerSerAlaThrTrpThrTyrSerProGlyProHisSerProAspAla 140
 Db 505 TCTCCATCACCGCATTCCCTCCACACCGACTACCCAGGCCACAGCTTGACGTG 564

Qy 141 SerPheGlnGlnSerSerThrAlaLysSerAlaLysSerAlaThrTrpThrTyrSerThrGluLeuLys 160
 Db 565 TCCTTCCAGAAGTCAGCAGGCCAAGTCCAGCTGGCCACCTGGACGTATTCCACTGAATGAG 624

Qy 161 LysLeutryrCysGlnIleAlaLysThrCysProIleGlnIleLysValMetThrProPro 180
 Db 625 AAACCTACTGCCAAATTGCAAAGCATGCCCATCAGGTGATGACCCACCT 684

Qy 181 ProGlnGlyAlaValIleAspGalanetProvaltryLysIysAlaGluIleValThrGlu 200
 Db 685 CCTCAGGGAGGTGTTATCGGCCATGCTGTCACAAAGTGGACGTGCGGG 744

Qy 201 ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyGlnIleAla 220
 Db 745 GTGGTCAAGGGTGGCTGCCAACATGAGCTGAGCCCTGAATTCAACGGGACAGATTGCC 804

Qy 221 ProProSerHisLeuIleArgValGluGlyAsnSerHisAlaGlnItyrValGluAspPro 240
 Db 805 CCTCTCTAGTCATTGATTCAGTGGAAACGCCATGCCACTATGAGANGATCCC 864

Qy 241 IleThrGlyArgGlnSerValLeuValProTyrGluProProGlnValGlyThrCluPhe 260
 Db 865 ATCACAGGAAAGACAGGTGCTGFACTCTATGACCAACCCAGGTGGCACTGAATTC 924

Qy 261 ThrThrValLeuLeuIleAspPheMetCysAsnSerSerCysValGlyGlyMetAsnArgArg 280
 Db 925 ACGAGCTCTTGACAAATTCTGTTACGAGTTGTTGGGATGAAACGCCCT 984

Qy 281 ProIleLeuIleIleValIleValGluIleValGluIleArgAspGlyGlnValLeuGlyArgArgCys 300
 Db 985 CCAATTAAATCATGTTACTCTGGAAACCAGAGATGGCCAACCTCTGGCCGAGCTCC 1044

Qy 301 PheIluAlaArgGlyCysAlaCysProGlyAspGlyAlaAspGluAspSerIle 320
 Db 1045 TTGGGCCGGATCTGCTGCTGCCAGAGCAGCAGGAAGGGATGAGATGACATC 1104

Qy 321 ArgLysGlnGlnValSerAspSerThrLysAsnGlyAspGlyThrLysArgProPheArg 340
 Db 1105 AGAAAAGCAGCAAGTTCTGAGCTAACAGAACGGTGAAGGCCCCCTTCTG 1164

Qy 341 GluAsnThrHisGlyIleGlnMetThrSerIleLysLysArgArgSerProAspAspGlu 360
 Db 1165 CAGAACACACATEGTCATCCAGATGACATCCATCAAGAACGAAAGATCCCCAGATGATGAA 1224

Qy 361 LeuLeuTyzLeuProValArgGlyArgGluIleUtyzLeuIleUtyzGlu 380
 Db 1225 CTGTTATACTTACAGTAGGGCCCTGAGACTTATGAAATGCTGTTGAGATCAAAGAG 1284

Qy 381 SerLeuGluLeuMetGlnIleLeuLeuProGlnHisIleIleLeuLeuProGlnGlnGln 400
 Db 1285 TCCCTGGAACTCATGAGTAATGCTACCTCTCAGCACAAATGAAAGTACAGGCAAAGGCA 1344

Qy 401 GluGlnGlnHisGlnHisIleLeuGluIleGluIleLeuLeuSerAlaCysPheArgAsnGlu 420
 Db 1345 CAGGAGCACCCGACACTTACTTCAGAAACATTCCTTCACTTCAGAA 1404

Qy 421 LeuValGluProArgArgGluIleProlysGluSerAspValPhePheArgHisSerLys 440
 Db 1405 CTTGGAGGCCCGAGAAACTCCAAACAACTCTGAGCTCTTCTAGACATTCCAG 1464

Db 1405 CCCCCAAACCGATCAGTGTACCCA 1488

Search completed: October 3, 2005, 06:22:31
 Job time : 971 secs

Result No.	Score	Query	Match	Length	DB ID	Description
1	2816	100.0	2816	9	US-09-735-705-333	Sequence 333, App
2	2816	100.0	2816	9	US-09-716A-333	Sequence 333, App
3	2816	100.0	2816	9	US-09-850-716A-333	Sequence 333, App
4	2816	100.0	2816	14	US-10-007-700-333	Sequence 333, App
5	2816	100.0	2816	15	US-10-117-982-333	Sequence 333, App
6	2816	100.0	2816	16	US-10-392-590-26	Sequence 26, App
7	2816	100.0	2816	16	US-10-393-590-64	Sequence 64, App
8	2816	100.0	2816	16	US-10-393-590-65	Sequence 65, App
9	2816	100.0	2816	16	US-10-393-597-26	Sequence 26, App
10	2816	100.0	2816	16	US-10-393-597-27	Sequence 27, App
11	2816	100.0	2816	16	US-10-393-597-64	Sequence 64, App
12	2816	100.0	2816	16	US-10-393-597-65	Sequence 65, App
13	2816	100.0	2816	16	US-10-394-087-26	Sequence 26, App
14	2816	100.0	2816	16	US-10-394-087-27	Sequence 27, App
15	2816	100.0	2816	16	US-10-394-087-64	Sequence 64, App
16	2816	100.0	2816	16	US-10-394-087-65	Sequence 65, App
17	2816	100.0	2816	16	US-10-394-087-65	Sequence 65, App
18	2816	100.0	2816	17	US-10-313-986-333	Sequence 333, App
19	2816	100.0	2816	20	US-10-715-972-333	Sequence 333, App
20	2816	100.0	2816	22	US-10-912-124-333	Sequence 333, App
21	1376	48.9	2270	9	US-09-735-705-332	Sequence 332, App
22	1376	48.9	2270	9	US-09-850-716A-332	Sequence 332, App
23	1376	48.9	2270	9	US-09-897-778-332	Sequence 332, App
24	1376	48.9	2270	14	US-10-007-700-332	Sequence 332, App
25	1376	48.9	2270	15	US-10-117-982-332	Sequence 332, App
26	1376	48.9	2270	17	US-10-313-986-332	Sequence 332, App
27	1376	48.9	2270	20	US-10-775-972-332	Sequence 332, App
28	1376	48.9	2270	22	US-10-912-124-332	Sequence 332, App
29	1365	48.5	4932	21	US-10-887-552A-596	Sequence 596, App
30	1364	48.4	4849	9	US-09-735-705-335	Sequence 335, App
31	1364	48.4	4849	9	US-09-850-716A-335	Sequence 335, App
32	1364	48.4	4849	9	US-09-897-778-335	Sequence 335, App
33	1364	48.4	4849	14	US-10-007-700-335	Sequence 335, App
34	1364	48.4	4849	15	US-10-117-982-335	Sequence 335, App
35	1364	48.4	4849	17	US-10-313-986-335	Sequence 335, App
36	1364	48.4	4849	18	US-10-240-425-1576	Sequence 1576, App
37	1364	48.4	4849	20	US-10-715-972-335	Sequence 335, App
38	1364	48.4	4849	22	US-10-912-124-335	Sequence 335, App
39	1347	47.8	1347	19	US-10-716-359-3	Sequence 3, App
40	1232	43.8	1551	9	US-09-735-705-337	Sequence 337, App
41	1232	43.8	1551	9	US-09-850-716A-337	Sequence 337, App
42	1232	43.8	1551	14	US-10-007-700-337	Sequence 337, App
43	1232	43.8	1551	15	US-10-117-982-337	Sequence 337, App
44	1232	43.8	1551	17	US-10-313-986-337	Sequence 337, App
45	1232	43.8	1551	17	US-10-313-986-337	Sequence 337, App

ALIGNMENTS

RESULT 1
US-09-735-705-333
; Sequence 333, Application US-09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongcong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy R.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Ajian
; APPLICANT: Steiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF LUNG CANCER
; FILE REFERENCE: 2.0121-45C14
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 333
; LENGTH: 2816
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-735-705-333

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	2816	100.0	2816	9	US-09-735-705-333	Sequence 333, App
2	2816	100.0	2816	9	US-09-850-716A-333	Sequence 333, App
3	2816	100.0	2816	9	US-09-897-778-333	Sequence 333, App
4	2816	100.0	2816	14	US-10-007-700-333	Sequence 333, App
5	2816	100.0	2816	15	US-10-117-982-333	Sequence 333, App
6	2816	100.0	2816	16	US-10-392-590-26	Sequence 26, App
7	2816	100.0	2816	16	US-10-393-590-27	Sequence 27, App

Query	Match	Score	DB	Length	2816;	Best Local Similarity	100.0%	Score	2816;	DB	9;	Length	2816;	
Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;														
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Qy	61 ACGACTCCCTGACCTTACATCCAGGTTTCGTTAGAAACCAGCTTCTTG	120	Qy	61 ACGACTCCCTGACCTTACATCCAGGTTTCGTTAGAAACCAGCTTCTTG	120	Qy	61 ACGACTCCCTGACCTTACATCCAGGTTTCGTTAGAAACCAGCTTCTTG	120	Qy	61 ACGACTCCCTGACCTTACATCCAGGTTTCGTTAGAAACCAGCTTCTTG	120	Qy	61 ACGACTCCCTGACCTTACATCCAGGTTTCGTTAGAAACCAGCTTCTTG	120
Db	1201 AAAGAAATTATTACCGATCCACATGTCAGCAGACAAGAACGTTCTAGT	180	Db	1201 AAAGAAATTATTACCGATCCACATGTCAGCAGACAAGAACGTTCTAGT	180	Db	1201 AAAGAAATTATTACCGATCCACATGTCAGCAGACAAGAACGTTCTAGT	180	Db	1201 AAAGAAATTATTACCGATCCACATGTCAGCAGACAAGAACGTTCTAGT	180	Db	1201 AAAGAAATTATTACCGATCCACATGTCAGCAGACAAGAACGTTCTAGT	180
Qy	1201 AAAGAAATTATTACCGATCCACATGTCAGCAGACAAGAACGTTCTAGT	180	Qy	1201 AAAGAAATTATTACCGATCCACATGTCAGCAGACAAGAACGTTCTAGT	180	Qy	1201 AAAGAAATTATTACCGATCCACATGTCAGCAGACAAGAACGTTCTAGT	180	Qy	1201 AAAGAAATTATTACCGATCCACATGTCAGCAGACAAGAACGTTCTAGT	180	Qy	1201 AAAGAAATTATTACCGATCCACATGTCAGCAGACAAGAACGTTCTAGT	180
Db	1261 CCAGGTTTCCAGCATPCTGGATTCTGGACAGCCATATGTTAGTTAGCC	240	Db	1261 CCAGGTTTCCAGCATPCTGGATTCTGGACAGCCATATGTTAGCC	240	Db	1261 CCAGGTTTCCAGCATPCTGGATTCTGGACAGCCATATGTTAGCC	240	Db	1261 CCAGGTTTCCAGCATPCTGGATTCTGGACAGCCATATGTTAGCC	240	Db	1261 CCAGGTTTCCAGCATPCTGGATTCTGGACAGCCATATGTTAGCC	240
Qy	241 ATTGACTTGAACTTGTGGATGACCATAGAAGATGGTGGACAAACAGATTGAGAT	300	Qy	241 ATTGACTTGAACTTGTGGATGACCATAGAAGATGGTGGACAAACAGATTGAGAT	300	Qy	241 ATTGACTTGAACTTGTGGATGACCATAGAAGATGGTGGACAAACAGATTGAGAT	300	Qy	241 ATTGACTTGAACTTGTGGATGACCATAGAAGATGGTGGACAAACAGATTGAGAT	300	Qy	241 ATTGACTTGAACTTGTGGATGACCATAGAAGATGGTGGACAAACAGATTGAGAT	300
Db	301 AGCATGGACTGTATCCGATGCGGACTGGACTCTGGACTCTGTAAGCAGTAC	360	Db	301 AGCATGGACTGTATCCGATGCGGACTGGACTCTGGACTCTGTAAGCAGTAC	360	Db	301 AGCATGGACTGTATCCGATGCGGACTGGACTCTGGACTCTGTAAGCAGTAC	360	Db	301 AGCATGGACTGTATCCGATGCGGACTGGACTCTGGACTCTGTAAGCAGTAC	360	Db	301 AGCATGGACTGTATCCGATGCGGACTGGACTCTGGACTCTGTAAGCAGTAC	360
Qy	361 ACCAACCTGGGTCTGAACACATGGACCCAGATTCAAAGCCTCTGGTCCAC	420	Qy	361 ACCAACCTGGGTCTGAACACATGGACCCAGATTCAAAGCCTCTGGTCCAC	420	Qy	361 ACCAACCTGGGTCTGAACACATGGACCCAGATTCAAAGCCTCTGGTCCAC	420	Qy	361 ACCAACCTGGGTCTGAACACATGGACCCAGATTCAAAGCCTCTGGTCCAC	420	Qy	361 ACCAACCTGGGTCTGAACACATGGACCCAGATTCAAAGCCTCTGGTCCAC	420
Db	421 AGTCCCTATAAACAGAACAGAACGGCAGAACAGGGTCAAGCAGCTACAG	480	Db	421 AGTCCCTATAAACAGAACAGAACGGCAGAACAGGGTCAAGCAGCTACAG	480	Db	421 AGTCCCTATAAACAGAACAGAACGGCAGAACAGGGTCAAGCAGCTACAG	480	Db	421 AGTCCCTATAAACAGAACAGAACGGCAGAACAGGGTCAAGCAGCTACAG	480	Db	421 AGTCCCTATAAACAGAACAGAACGGCAGAACAGGGTCAAGCAGCTACAG	480
Qy	481 CCCAGCTCACCTTGATGCTCTCPCTCATACCCCCTAACACCGTAC	540	Qy	481 CCCAGCTCACCTTGATGCTCTCPCTCATACCCCCTAACACCGTAC	540	Qy	481 CCCAGCTCACCTTGATGCTCTCPCTCATACCCCCTAACACCGTAC	540	Qy	481 CCCAGCTCACCTTGATGCTCTCPCTCATACCCCCTAACACCGTAC	540	Qy	481 CCCAGCTCACCTTGATGCTCTCPCTCATACCCCCTAACACCGTAC	540
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Qy	601 TGACGTTATCCACTGAACTGTGAACTTGTGAACTTGTGAACTTGT	660	Qy	601 TGACGTTATCCACTGAACTGTGAACTTGTGAACTTGTGAACTTGT	660	Qy	601 TGACGTTATCCACTGAACTGTGAACTTGTGAACTTGTGAACTTGT	660	Qy	601 TGACGTTATCCACTGAACTGTGAACTTGTGAACTTGTGAACTTGT	660	Qy	601 TGACGTTATCCACTGAACTGTGAACTTGTGAACTTGTGAACTTGT	660
Db	661 CAGATCAAGGTGATGACCCACCTCTGGAGCTTATCGGCCATGCTG	720	Db	661 CAGATCAAGGTGATGACCCACCTCTGGAGCTTATCGGCCATGCTG	720	Db	661 CAGATCAAGGTGATGACCCACCTCTGGAGCTTATCGGCCATGCTG	720	Db	661 CAGATCAAGGTGATGACCCACCTCTGGAGCTTATCGGCCATGCTG	720	Db	661 CAGATCAAGGTGATGACCCACCTCTGGAGCTTATCGGCCATGCTG	720
Qy	721 AAAAAGCTGAGGACGTCAGGAGGGTGTGAAGCGGTSCCCAAACCATG	780	Qy	721 AAAAAGCTGAGGACGTCAGGAGGGTGTGAAGCGGTSCCCAAACCATG	780	Qy	721 AAAAAGCTGAGGACGTCAGGAGGGTGTGAAGCGGTSCCCAAACCATG	780	Qy	721 AAAAAGCTGAGGACGTCAGGAGGGTGTGAAGCGGTSCCCAAACCATG	780	Qy	721 AAAAAGCTGAGGACGTCAGGAGGGTGTGAAGCGGTSCCCAAACCATG	780
Db	781 GATTCACAGGGACAGATTGAGATCTTGTGAACTTGTGAACTTGT	840	Db	781 GATTCACAGGGACAGATTGAGATCTTGTGAACTTGTGAACTTGT	840	Db	781 GATTCACAGGGACAGATTGAGATCTTGTGAACTTGTGAACTTGT	840	Db	781 GATTCACAGGGACAGATTGAGATCTTGTGAACTTGTGAACTTGT	840	Db	781 GATTCACAGGGACAGATTGAGATCTTGTGAACTTGTGAACTTGT	840
Qy	841 CATGCCCAAGTGTGGCACTGAAATTGCAAGGAGCTTGTGAACTTGT	900	Qy	841 CATGCCCAAGTGTGGCACTGAAATTGCAAGGAGCTTGTGAACTTGT	900	Qy	841 CATGCCCAAGTGTGGCACTGAAATTGCAAGGAGCTTGTGAACTTGT	900	Qy	841 CATGCCCAAGTGTGGCACTGAAATTGCAAGGAGCTTGTGAACTTGT	900	Qy	841 CATGCCCAAGTGTGGCACTGAAATTGCAAGGAGCTTGTGAACTTGT	900
Db	901 CCACCCCCAGGGACAGATTGAGATCTTGTGAACTTGTGAACTTGT	960	Db	901 CCACCCCCAGGGACAGATTGAGATCTTGTGAACTTGTGAACTTGT	960	Db	901 CCACCCCCAGGGACAGATTGAGATCTTGTGAACTTGTGAACTTGT	960	Db	901 CCACCCCCAGGGACAGATTGAGATCTTGTGAACTTGTGAACTTGT	960	Db	901 CCACCCCCAGGGACAGATTGAGATCTTGTGAACTTGTGAACTTGT	960
Qy	961 TTGTGTTGGGGATGAACTGCTTGCCTTCAGGCGGGATCTGTC	1020	Qy	961 TTGTGTTGGGGATGAACTGCTTGCCTTCAGGCGGGATCTGTC	1020	Qy	961 TTGTGTTGGGGATGAACTGCTTGCCTTCAGGCGGGATCTGTC	1020	Qy	961 TTGTGTTGGGGATGAACTGCTTGCCTTCAGGCGGGATCTGTC	1020	Qy	961 TTGTGTTGGGGATGAACTGCTTGCCTTCAGGCGGGATCTGTC	1020
Db	1021 GGCGCAAGTCCTGGCCAGCGCTGCTGCCAGAAGGAC	1080	Db	1021 GGCGCAAGTCCTGGCCAGCGCTGCTGCCAGAAGGAC	1080	Db	1021 GGCGCAAGTCCTGGCCAGCGCTGCTGCCAGAAGGAC	1080	Db	1021 GGCGCAAGTCCTGGCCAGCGCTGCTGCCAGAAGGAC	1080	Db	1021 GGCGCAAGTCCTGGCCAGCGCTGCTGCCAGAAGGAC	1080

Db	2101	TTCGTGAGAACCTTGCAATTATTGGTGTCCCTCATGTTAGGAAATTTCTTAAT	2160		1	TCGTGTATCAAAGACAGTGTGAAGAAATGAAATTGCAACTTCACGGTGTGCCACCT	60
Qy	2161	GCTGTGTCACCTGCCCCACTGTATGTTGGCATTGTGTATGCTAAGATTTCTTGTAA	2220	Db	61	ACAGTACTGCCTCACCCCTTACATCAGGGTTTGTAGAAACCCNGCTCATTTCTTGG	120
Db	2161	GCTGTGTCACCTGCCCCACTGTATGTTGGCATTGTGTATGCTAAGATTTCTTGTAA	2220	Qy	61	ACAGTACTGCCTCACCCCTTACATCAGGGTTTGTAGAAACCCNGCTCATTTCTTGG	120
Db	2221	CATGAAACCTGGAAAGACCTACTACAAAAAAACTGTTGGCCCCATAGCAGGTGAA	2280	Db	121	AAAGAAAGTTTACCGATTCACCATGTCAGAGCACAGAACATGAATTCCCTCAGT	180
Qy	2221	CATGAAACCTGGAAAGACCTACTACAAAAAAACTGTTGGCCCCATAGCAGGTGAA	2280	Qy	121	AAAGAAAGTTTACCGATTCACCATGTCAGAGCACAGAACATGAATTCCCTCAGT	180
Db	2281	CTCAATTGGCTTTAATGAAAGCAAACTCAACCCAGTAAATTGGCTTAGTGT	2340	Db	121	AAAGAAAGTTTACCGATTCACCATGTCAGAGCACAGAACATGAATTCCCTCAGT	180
Qy	2281	CTCAATTGGCTTTAATGAAAGCAAACTCAACCCAGTAAATTGGCTTAGTGT	2340	Qy	181	CCAGGGTTTCCAGCATATCTGGATTTCAGGCTATAATGTTCACTTCAGCCC	240
Db	2341	TGTTTACCAATTTCAGCAAGCTCAAATAGAAATTGAAACCCCTTCACAAAATCTGTGATT	2400	Db	181	CCAGGGTTTCCAGCATATCTGGATTTCAGGCTATAATGTTCACTTCAGCCC	240
Qy	2341	TGTTTACCAATTTCAGCAAGCTCAAATAGAAATTGAAACCCCTTCACAAAATCTGTGATT	2400	Qy	241	ATTGACTGAACTTTGTGATGAAACATAGAAAGATGGTGGCGAACAAACAGATGGATT	300
Db	2401	AATTGCTTATTAGAGCTCTATCCCTCAAGCTTACCCATAAAACGCCATATA	2460	Db	241	ATTGACTGAACTTTGTGATGAAACATAGAAAGATGGTGGCGAACAAACAGATGGATT	300
Qy	2401	AATTGCTTATTAGAGCTCTATCCCTCAAGCTTACCCATAAAACGCCATATA	2460	Qy	301	AGCATGGACTGTATCGATGACCTGGACCTGGTGGCCAGACTGGTGGCCAGAGTAC	360
Db	2461	CTGATACTGGTCAATTAGCCAGGAGACTTACGTTGAGTAAGTCCAAGC	2520	Db	301	AGGACCTGGGCTCTGAACAGCATGGACCAGATTAGAAGGGCTCTCGTCCACC	360
Qy	2461	CTGATACTGGTCAATTAGCCAGGAGACTTACGTTGAGTAAGTCCAAGC	2520	Qy	361	ACGAAACCTGGGCTCTGAACAGCATGGACCAGATTAGAAGGGCTCTCGTCCACC	420
Db	2461	CTGATACTGGTCAATTAGCCAGGAGACTTACGTTGAGTAAGTCCAAGC	2520	Db	361	ACGAAACCTGGGCTCTGAACAGCATGGACCAGATTAGAAGGGCTCTCGTCCACC	420
Qy	2522	AGACGTGTTAAATACGCACTCCGGACTGGAAAGTTAAAGATGGAAAGGGTAGACTCT	2580	Qy	421	AGTCCTATAACAGACCAAGCGCCAGAACGGCTCACCGGCCATCCGCCTAACACAG	480
Db	2522	AGACGTGTTAAATACGCACTCCGGACTGGAAAGTTAAAGATGGTAGACTCT	2580	Db	421	AGTCCTATAACAGACCAAGCGCCAGAACGGCTCACCGGCCATCCGCCTAACACAG	480
Qy	2581	TTCTTTTTTACTCAAAAGTTAGAAATCTCGTTCTTCATTTAAACATATT	2640	Qy	481	CCCAAGCTCCACCTTGTGATCTCTCATCACCCCTCCACACCCACTAC	540
Db	2581	TTCTTTTTTACTCAAAAGTTAGAAATCTCGTTCTTCATTTAAACATATT	2640	Db	481	CCCAAGCTCCACCTTGTGATCTCTCATCACCCCTCCACACCCACTAC	540
Qy	2641	TTAAGATAATAGCATAAAGACTTTAAAGTTCTCCCACTTCCACACCCAGT	2700	Qy	541	CCAGCCCCGACACTTGCAGGTGCTCCAGAGTCAGACCCAGTGCGCCACC	600
Db	2641	TTAAGATAATAGCATAAAGACTTTAAAGTTCTCCCACTTCCACACCCAGT	2700	Db	541	CCAGCCCCGACACTTGCAGGTGCTCCAGAGTCAGTGCAGCCAAAGTCGCCACC	600
Qy	2701	CACCAAGCATGTTATTCTGTCACCAAGAAATGTTGCACTTGTGTTAAAGAAA	2816	Qy	661	CAGATCAAGTGTGATGAACTCCACCTCTCAGGGACCTGTATCCGGCCATGCCCTCTTAC	720
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Qy	2761	TTGTGTGATGTTGTTGATTTTCAATTTCATTTCAATTAACCTTTGCACTTGTGTTAAAGAAA	2816	Db	721	AAAAAAGCTGAGGGAAAGTGGGACTGTTGATCTAGTCAATTGCAAGTAAAGGAGCT	780
Db	2761	TTGTGTGATGTTGTTGATTTTCAATTTCATTTCAATTAACCTTTGCACTTGTGTTAAAGAAA	2816	Db	721	AAAAAAGCTGAGGGAAAGTGGGACTGTTGATCTAGTCAATTGCAAGTAAAGGAGCT	780
RESULT 2				Qy	781	CATGCCCACTATGTAAGATCCATCACGGAGAACATGAGCTGAGGCCGT	840
US-09-850-716A-333				Qy	781	GAATTCAGGGGAACTTGTGATGCCCTCTAGTCAATTGCAAGTAAAGGAGCT	840
Patent No. US20020115139A1				Qy	781	GAATTCAGGGGAACTTGTGATGCCCTCTAGTCAATTGCAAGTAAAGGAGCT	840
GENERAL INFORMATION:				Qy	841	CATGCCCACTATGTAAGATCCATCACGGAGAACATGAGCTGAGGCCGT	900
APPLICANT: McNeill, Michael D.				Qy	841	CATGCCCACTATGTAAGATCCATCACGGAGAACATGAGCTGAGGCCGT	900
APPLICANT: Rettler, Marc W.				Db	901	CCACCCCACTGTTGGCAACTGAATTCAAGCAGTCTGTGAGTTCAACCCAGT	960
APPLICANT: Kalos, Michael D.				Db	901	CCACCCCACTGTTGGCAACTGAATTCAAGCAGTCTGTGAGTTCAACCCAGT	960
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY				Db	901	CCACCCCACTGTTGGCAACTGAATTCAAGCAGTCTGTGAGTTCAACCCAGT	960
FILE REFERENCE: 210121.455C15				Qy	961	TGTGTGAGGGGAACTTGTGATGCCCTCTAGTCAATTGCAAGTAAAGGAGCT	1020
CURRENT APPLICATION NUMBER: US/09/850,716A				Db	961	TGTGTGAGGGGAACTTGTGATGCCCTCTAGTCAATTGCAAGTAAAGGAGCT	1020
CURRENT FILING DATE: 2001-05-07				Qy	1081	AGGAGGGGAACTGAGGATAGCATGAAAGCAGAAGTGGAGAAGTACAAGAGGT	1140
NUMBER OF SEQ ID NOS: 440				Qy	1081	AGGAGGGGAACTGAGGATAGCATGAAAGCAGAAGTGGAGAAGTACAAGAGGT	1140
SOFTWARE: FastSEQ for Windows Version 3.0							
SEQ ID NO: 333							
LENGTH: 2816							
TYPE: DNA							
ORGANISM: Homo sapiens							
US-09-850-716A-333							
Query Match 100.0 %				Qy	1021	GGGAAGTCTGGCCGAGGCTGTTGAGCCCGGATCTGCTTGCCAGGAAGAC	1080
Best Local Similarity 100.0 %				Db	1021	GGGAAGTCTGGCCGAGGCTGTTGAGCCCGGATCTGCTTGCCAGGAAGAC	1080
Matches 2816; Conservative 0;				Qy	1081	AGGAGGGGAACTGAGGATAGCATGAAAGCAGAAGTGGAGAAGTACAAGAGGT	1140

1081	AGGAAGGGGATGAGATAATGATCAGAAAGGAGCAAGTTCGACAGTAAAGAACGGT	1140	Qy	2221	CATGAACCCCTGGAAAGACCTACTACAAAAAAACTGTTGGCCCCATAGCAGGTGAA	2280	
1141	GATGGTACGAAGGCCGTTTCGTCAAGAACACACATGGTATCCGATGACATCCATCAAG	1200	D _b	2221	CATGAACCCCTGGAAAGACCTACTACAAAAAACTGTTGGCCCCATAGCAGGTGAA	2280	
1141	GATGGTACGAAGGCCGTTTCGTCAAGAACACACATGGTATCCGATGACATCCATCAAG	1200	Y	2281	CTCATTTGTGTTTAATAGAAAAGACAATCCACCCAGTAATATGCCCTTAGTGTACT	2340	
1201	AAACGAGATCCCAGATGAGAACTGTTAATCTTACCGTGAGGGCCGAGACTT	1260	D _b	2281	CTCATTTGTGTTTAATAGAAAAGACAATCCACCCAGTAATATGCCCTTAGTGTACT	2340	
1201	AAACGAGATCCCAGATGAGAACTGTTAATCTTACCGTGAGGGCCGAGACTT	1260	o	Qy	2241	TGTTTACCATATTCAAGCTTAAATAGAATTGAGGTTGAGCCCTCTCACAAAATCTGTGATT	2400
1261	GAAATSCTGTGAGATAAGATCAAGAGTCCCTGGAACTCATGGAGTACCTTCAGCACACA	1320	D _b	2341	TGTTTACCATATTCAAGCTTAAATAGAATTGAGGTTGAGCCCTCTCACAAAATCTGTGATT	2400	
1261	GAAATSCTGTGAGATAAGATCAAGAGTCCCTGGAACTCATGGAGTACCTTCAGCACACA	1320	y	Qy	2401	AATTGGCTTAATTAGACTCTTATCCCTAACGCTACCTACCAAAACCCTATTAA	2460
1321	ATTGAAACGTACAGGCAACAGCAACAGCAGCACCTTACCTCAAGAACATCTC	1380	D _b	2401	AATTGGCTTAATTAGACTCTTATCCCTAACGCTACCTACCAAAACCCTATTAA	2460	
1321	ATTGAAACGTACAGGCAACAGCAACAGCAGCACCTTACCTCAAGAACATCTC	1380	b	Qy	2461	CTGATACGTGTTAGTCGATTTAGCCAGGAGACTTACGGTTAGTGAAGTCAAGC	2520
1381	CTTCAGCCGCTTCAGGATGAGCTTGTAGGCCGGAGAAACTCCAAACATCT	1440	D _b	2461	CTGATACGTGTTAGTCGATTTAGCCAGGAGACTTACGGTTAGTGAAGTCAAGC	2520	
1381	CTTCAGCCGCTTCAGGATGAGCTTGTAGGCCGGAGAAACTCCAAACATCT	1440	Y	Qy	2521	AGACGTTTAATCTGGACTCTGGACTTGGAAATAAGATGAAAGGTGACACTT	2580
1441	GACGTGTTCTTTAGACATTTAGACATCCAGGCCAACCGATCATGGTACCCATAGGCCCTATC	1500	D _b	2521	AGACGTTTAATCTGGACTCTGGACTTGGAAATAAGATGAAAGGTGACACTT	2580	
1441	GACGTGTTCTTTAGACATCCAGGCCAACCGATCATGGTACCCATAGGCCCTATC	1500	o	Qy	2581	TTCTTCTTACTCAAAGTTAGAAGATCTCTGTTCTTCATTTAAACACATT	2640
1501	TCTATATTAACTGTGTTGTTATTCCTGATGTTATGTTGACTGTGTTGCTGTA	1560	D _b	2581	TTCTTCTTACTCAAAGTTAGAAGATCTCTGTTCTTCATTTAAACACATT	2640	
1501	TCTATATTAACTGTGTTGTTATTCCTGATGTTATGAGCTTGTGAGCCCTCATAGA	1560	Y	Qy	2641	TTAAGATAATGGATAAACGTTTAATTTCTCCCTCCATCTCCACCCACT	2700
1561	TGTGTTGCTGTTGATCTACCCCTCATAAACAGGACTTGAAGACACTTGCTAGAGA	1620	D _b	2641	TTAAGATAATGGATAAACGTTTAATTTCTCCCTCCATCTCCACCCACT	2700	
1561	TGTGTTGCTGTTGATCTACCCCTCATAAACAGGACTTGAAGACACTTGCTAGAGA	1620	o	Qy	2701	CACCGAACGACTTATTCGTCACCAAGACATACTTCTGGTTAGGCTGTGCTT	2760
1621	CCCCACTGTCAAAGGCCAACAGCCACTTGTGAGAACTTCTTGGACTCAAACCT	1680	D _b	2701	CACCGAACGACTTATTCGTCACCAAGACATGTTCTGGTTAGGCTGTGCTT	2760	
1621	CCCCACTGTCAAAGGCCAACAGCCACTTGTGAGAACTTCTTGGACTCAAACCT	1680	Y	Qy	2761	TTGTGGATGTGTTGATTAAATTCTCAATAAACTTTGATCTTGGTTAAAGAAA	2816
1681	TTACAGAAAGGATGTTCTCGAGATTCTGATCTTCTAACCGCCATCTGGGGTAG	1740	D _b	2761	TTGTGGATGTGTTGATTAAATTCTCAATAAACTTTGATCTTGGTTAAAGAAA	2816	
1681	TTACAGAAAGGATGTTCTCGAGATTCTGATCTTCTAACCGCCATCTGGGGTAG	1740	o	Qy	1741	GAACCACTGTGTTGCTGATGTTCTGGAGGGAGGGTAGGGTCAGGGG	1800
1741	GAACCACTGTGTTGCTGATGTTCTGGAGGGAGGGTAGGGTCAGGGG	1800	Y	1741	GAACCACTGTGTTGCTGATGTTCTGGAGGGAGGGTAGGGTCAGGGG	1800	
1801	GAAAGGGCCTTAAAGATGTTTATGGAAACCTTCTGTTCTGTTCTGGAGGGAGGGTAGGG	1860	Y	1801	GAAAGGGCCTTAAAGATGTTTATGGAAACCTTCTGTTCTGTTCTGGAGGGAGGGTAGGG	1860	
1801	GAAAGGGCCTTAAAGATGTTTATGGAAACCTTCTGTTCTGTTCTGGAGGGAGGGTAGGG	1860	o	Qy	1861	AATTACAGGGAAAGCTTGTAGGAGCTCAACCTTAAGATGTTCTTAAAGAAAAGGAG	1920
1861	AATTACAGGGAAAGCTTGTAGGAGCTCAACCTTAAGATGTTCTTAAAGAAAAGGAG	1920	Y	1861	AATTACAGGGAAAGCTTGTAGGAGCTCAACCTTAAGATGTTCTTAAAGAAAAGGAG	1920	
1921	AAAAAAGTGTATGTGCTGATTAATATTCGAATAGTGAAGTGTAGGTGACTGAGAGCTCAGTCAGA	1980	Y	1921	CCCCTTTAATGCTGGTCATTAATATTCGAATAGTGAAGTGTAGGTGACTGAGAGCTCAGTCAGA	2040	
1921	AAAAAAGTGTATGTGCTGATTAATATTCGAATAGTGAAGTGTAGGTGACTGAGAGCTCAGTCAGA	1980	o	Qy	1981	CCCCTTTAATGCTGGTCATTAATATTCGAATAGTGAAGTGTAGGTGACTGAGAGCTCAGTCAGA	2040
1981	CCCCTTTAATGCTGGTCATTAATATTCGAATAGTGAAGTGTAGGTGACTGAGAGCTCAGTCAGA	2040	Y	1981	CCCCTTTAATGCTGGTCATTAATATTCGAATAGTGAAGTGTAGGTGACTGAGAGCTCAGTCAGA	2100	
2041	TACTGCTGGAGCGAGGTGATCATACCAAAGTAATCAACTTAAGTGTAGGTGACTGAGAGCTCAGTCAGA	2100	D _b	2041	TACTGCTGGAGCGAGGTGATCATACCAAAGTAATCAACTTAAGTGTAGGTGACTGAGAGCTCAGTCAGA	2100	
2041	TACTGCTGGAGCGAGGTGATCATACCAAAGTAATCAACTTAAGTGTAGGTGACTGAGAGCTCAGTCAGA	2100	Y	Qy	2101	TTGTGAGAACTTGCACTGTGTTCTCCCTCATGTGTTCTCCCTCATGTGAACTTCTTAAT	2160
2101	TTGTGAGAACTTGCACTGTGTTCTCCCTCATGTGTTCTCCCTCATGTGAACTTCTTAAT	2160	o	Qy	2101	TTGTGAGAACTTGCACTGTGTTCTCCCTCATGTGAACTTCTTAAT	2160
2161	GCTGTTACCTGCCCTGCACACTGTATGTTGGCATCTGTATGCTAAAGTTCTTGTAA	2220	Y	2161	GCTGTTACCTGCCCTGCACACTGTATGTTGGCATCTGTATGCTAAAGTTCTTGTAA	2220	
2161	GCTGTTACCTGCCCTGCACACTGTATGTTGGCATCTGTATGCTAAAGTTCTTGTAA	2220	o	Qy	US-09-897-778-333	Query Match	100.0%
				US-09-897-778-333	Best Local Similarity	100.0%	
				US-09-897-778-333	Pred. No.	0;	
				US-09-897-778-333	Mismatches	0;	
				US-09-897-778-333	Indels	0;	
				US-09-897-778-333	Gaps	0;	

Db	2161	GCTGTGTAACCTGCCACTGTATGTGGATCTGTATGCTAANGTTTCTGTGA	2220	; LENGTH: 2816
Oy	2221	CATGAAACCCTGGAAAGACCTACTACAAAAAAAAACTGTTGGCCCCATAGCCAGGTGA	2280	; TYPE: DNA
Db	2221	CATGAAACCCTGGAAAGACCTACTACAAAAAAAACTGTTGGCCCCATAGCCAGGTGA	2280	; ORGANISM: Homo sapiens
Qy	2281	CTCATTTGCTGCTTTAATAGAAAGACAATCACCCTAACGTAATATGCCCTAACGTAGT	2340	; US-10-007-700-333
Db	2281	CTCATTTGCTGCTTTAATAGAAAGACAATCACCCTAACGTAATATGCCCTAACGTAGT	2340	
Qy	2341	TGTTTACATTAACTCAAGCTCAAATAGAAATTGAAACCCCTCTCACAAATCTGTGAT	2400	Query Match 100.0%; Score 2816; Length 2816;
Db	2341	TGTTTACATTAACTCAAGCTCAAATAGAAATTGAAACCCCTCTCACAAATCTGTGAT	2400	Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Qy	2401	AATTGCTTAATTAGAGCTTCACTCCCTAACCTACCAAAACAGCCATATA	2460	Matches 2816; Conservative 0;
Db	2401	AATTGCTTAATTAGAGCTTCACTCCCTAACCTACCAAAACAGCCATATA	2460	
Qy	2461	CTGATACGTTCACTGCATTAGCCAGGAAGCTAACCTACGTTGAGTAAGTCAGC	2520	Query Match 100.0%; Score 2816; Length 2816;
Db	2461	CTGATACGTTCACTGCATTAGCCAGGAAGCTAACCTACGTTGAGTAAGTCAGC	2520	Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Qy	2521	AGACGTGTTAAATCGACCTCTGGACTGGTAGACTACT	2580	Matches 2816; Conservative 0;
Db	2521	AGACGTGTTAAATCGACCTCTGGACTGGTAGACTACT	2580	
Qy	2581	TTCCTTTTTTACTCAAAGTTAGAGAAATCTCTGTTTCATTTAACACATATT	2640	Query Match 100.0%; Score 2816; Length 2816;
Db	2581	TTCCTTTTTTACTCAAAGTTAGAGAAATCTCTGTTTCATTTAACACATATT	2640	Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Qy	2641	TAAAGATAATAGATAAAGACTTTAAAATGTTGTCCTCCATCTTCCCACACCCAGT	2700	Query Match 100.0%; Score 2816; Length 2816;
Db	2641	TAAAGATAATAGATAAAGACTTTAAAATGTTGTCCTCCATCTTCCCACACCCAGT	2700	Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Qy	2701	CACCGCACTGTTATTCTGTACCAAGAACATGATTCTTATGAGGTGTTGCT	2760	Query Match 100.0%; Score 2816; Length 2816;
Db	2701	CACCGCACTGTTATTCTGTACCAAGAACATGATTCTTATGAGGTGTTGCT	2760	Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Qy	2761	TGTGGATGTTGTTGATTTCATAATAACCTTTGGCTCTGGTTAAAGAAA	2816	Query Match 100.0%; Score 2816; Length 2816;
Db	2761	TGTGGATGTTGTTGATTTCATAATAACCTTTGGCTCTGGTTAAAGAAA	2816	Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
<hr/>				
RESULT 4				
US-10-007-700-333				
Sequence 333, Application US-10007700				
GENERAL INFORMATION:				
APPLICANT: Wang, Tongtong				
APPLICANT: Shekaly, Yasir A.W.				
APPLICANT: Li, Samuel X.				
APPLICANT: Kalos, Michael D.				
APPLICANT: Henderson, Robert A.				
APPLICANT: McNeill, Patricia D.				
APPLICANT: Carter, Derrick				
APPLICANT: Watanabe, Yoshinori				
APPLICANT: Peckman, David W.				
APPLICANT: Cai, Feng				
APPLICANT: Foy, Teresa M.				
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY				
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER				
FILE REFERENCE: 210121-455C17				
CURRENT APPLICATION NUMBER: 2001-11-30				
CURRENT FILING DATE: 2001-11-30				
NUMBER OF SEQ ID NOS: 459				
SOFTWARE: FastSEQ for Windows Version 4.0				
SEQ ID NO 333				

QY	961	TGTGTTGGGGATAACCCCGTCAATTATCATTTACTCTGAAACCAGAGT	1020		Db	2041	TACTCTGGCAGGAGTCATTTACCAAAAAGTAATCATTACCTTGTAGGAGACTTGTGGGGAGAGTC	2100
Db	961	TGTGTTGGGGATAACCCCGTCAATTATCATTTACTCTGAAACCAGAGT	1020		Qy	2101	TGTGAGACTTGATTATTGTGTCCTCCCTATGTAGGATAGACATTCTTAAT	216
Qy	1021	GGCAAAGTCTGGGGACCGTGTGTTGAGGCCGATCTGCTGGCCAGGAGAC	1080		Db	2101	TGTGAGACTTGTGCTGGCCACTGTGTTCTGCTGGCCATCTGCTGGCCAGGAGAC	216
Db	1021	GGCAAAGTCTGGGGACCGTGTGTTGAGGCCGATCTGCTGGCCAGGAGAC	1080		Qy	2161	GCTGTTACTGGCCTGCCCCTGCACTGTGTTATGCTGGCACTGTTCTGTGA	2222
Qy	1081	AGGAAGGGGGATGAAGATAGCATAGAAAGCAGTTGGACAGTACAAGAACGCT	1140		Db	2161	GCTGTTACTGGCCTGCCCCTGCACTGTGTTATGCTGGCACTGTTCTGTGA	2222
Db	1081	AGGAAGGGGGATGAAGATAGCATAGAAAGCAGTTGGACAGTACAAGAACGCT	1140		Qy	2221	CATGAAACCCGTTGGAAAGACCTACTACAAAAAAACTGTTGTTGGCCCCATAGCAGCTGAA	228
Qy	1141	GATGGTACAGGGCCGTTCTGCTAGAAACACATGGPATCGCATCCATCAG	1200		Db	2221	CATGAAACCCGTTGGAAAGACCTACTACAAAAAAACTGTTGTTGGCCCCATAGCAGCTGAA	228
Db	1141	GATGGTACAGGGCCGTTCTGCTAGAAACACATGGPATCCATCAG	1200		Qy	2281	CTCATTTGTGCTTTAATAGAAACAAATCCACCCAGTAATTGCGCTTAGTGTAGT	234
Qy	1201	AAACGAAAGTCCCAAGATGATACTTACCATGCTGAGCTTACATCAG	1260		Db	2281	CTCATTTGTGCTTTAATAGAAACAAATCCACCCAGTAATTGCGCTTAGTGTAGT	234
Db	1201	AAACGAAAGTCCCAAGATGATACTTACCATGCTGAGCTTACATCAG	1260		Qy	2341	TGTTTACCTTAAAGTCATAAAATAGAATTGAAAGCTCAGAAAATCTGTGATT	2400
Qy	1261	GAATGCTGTTGAGATCAAAAGACTCCCTGGAAACTCATGGACTTACCTGAGAC	1320		Db	2341	TGTTTACCTTAAAGTCATAAAATAGAATTGAAAGCTCAGAAAATCTGTGATT	2400
Db	1261	GAATGCTGTTGAGATCAAAAGACTCCCTGGAAACTCATGGACTTACCTGAGAC	1320		Qy	2401	AATTGCTTAATTAGAGCTTCTATCCCTGAGCCATTACCTTACCCATTATA	246
Qy	1321	ATTGAAACGTAAGCCACAGGACCCAGCAAGCCTACTTGAAGAACATTC	1380		Db	2401	AATTGCTTAATTAGAGCTTCTATCCCTGAGCCATTACCTTACCCATTATA	246
Db	1321	ATTGAAACGTAAGCCACAGGACCCAGCAAGCCTACTTGAAGAACATTC	1380		Qy	2461	CTGATACTGTTCACTGCATTAGCGAGGAGACTTACGTGTTTGAGTAAGTGAATCCAAGC	252
Qy	1381	CTTCAGCTGCTCTCAGGATGAGCTTGTGAGGCCGGAGAGAACTCAGAACTT	1440		Db	2461	CTGATACTGTTCACTGCATTAGCGAGGAGACTTACGTGTTTGAGTAAGTGAATCCAAGC	252
Db	1381	CTTCAGCTGCTCTCAGGATGAGCTTGTGAGGCCGGAGAGAACTCAGAACTT	1440		Qy	2521	AGACCTGTTAAATAGGACTCCCTGACTCTGAAATAAGATTGAAGGGTAGATCTACTT	258
Qy	1441	GACGCTCTTCTTGTGAGATTCAGGAAAGCCGATCTGTGATCCATAGAGCCCTATC	1500		Db	2521	AGACCTGTTAAATAGGACTCCCTGACTCTGAAATAAGATTGAAGGGTAGATCTACTT	258
Db	1441	GACGCTCTTCTTGTGAGATTCAGGAAAGCCGATCTGTGATCCATAGAGCCCTATC	1500		Qy	2581	TTCCTTTTACTCAAAAGTTAGAGAACTCTCTGTTCTTCACTTTAAACATATT	264
Qy	1501	TCTATATTAAAGTGTGTTATTCTCATGTGATATGCTAGTGTGTGTGTGT	1560		Db	2581	TTCCTTTTACTCAAAAGCTTAAATGTTAGAGAACTCTCTGTTCTTCACTTTAAACATATT	264
Db	1501	TCTATATTAAAGTGTGTTATTCTCATGTGATATGCTAGTGTGTGTGTGT	1560		Qy	2641	TTAGATAATAGCATTAAGACTTTAAATGTTCTCCCTCCATCTTCCACACCCAGT	270
Qy	1561	TGTGTTGGCTGTGTATCTAGCCCTCATAAAGACTGAGACTTGTGTCAGAGA	1620		Db	2641	TTAGATAATAGCATTAAGACTTTAAATGTTCTCCCTCCATCTTCCACACCCAGT	270
Db	1561	TGTGTTGGCTGTGTATCTAGCCCTCATAAAGACTGAGACTTGTGTCAGAGA	1620		Qy	2701	CACCGCACTGTATTCTGTCACTAAGAGCAATGTTCTGTGTTAGGGCTGTGCTT	276
Qy	1621	CCCAACTGCTCAAGGCACAAAGGCAACTAGTGAGAGAAATCTTGACCTGAAACCT	1680		Db	2701	CACCGCACTGTATTCTGTCACTAAGAGCAATGTTCTGTGTTAGGGCTGTGCTT	276
Db	1621	CCCAACTGCTCAAGGCACAAAGGCAACTAGTGAGAGAAATCTTGACCTGAAACCT	1680		Qy	2761	TTGCTGATCTGTGATTTAAATTCTCAATAAAACTTTGCATCTTGGTTAAAGAAA	2816
Qy	1681	TTACAGAAAGGAGTTCTGCAATTGCTGAGTTGCTGAGCTTGTGTCAGAG	1740		Db	2761	TTGCTGATCTGTGATTTAAATTCTCAATAAAACTTTGCATCTTGGTTAAAGAAA	2816
Db	1681	TTACAGAAAGGAGTTCTGCAATTGCTGAGTTGCTGAGCTTGTGTCAGAG	1740		RESULT 5			
Qy	1741	GAACCACTGTTCTGTGAGCTTCTGTGAGCTTCTGTGTCAGGTGGG	1800			US-10-117-982-333		
Db	1741	GAACCACTGTTCTGTGAGCTTCTGTGTCAGGTGGG	1800			Sequence 333, Application US/10117982		
Qy	1801	GAAGGGGGATTAGATGTATTGAAACCCCTTCTGCTTCTGTGTCATTA	1860			Publication No. US20030138438A1		
Db	1801	GAAGGGGGATTAGATGTATTGAAACCCCTTCTGCTTCTGTGTCATTA	1860			GENERAL INFORMATION:		
Qy	1861	AATTACAGGAAAGTTTGAGCAGGTCTCAACTTAAGATGCTTCTGTGTCATTA	1920			APPLICANT: Poy, Teresa M.		
Db	1861	AATTACAGGAAAGTTTGAGCAGGTCTCAACTTAAGATGCTTCTGTGTCATTA	1920			APPLICANT: Fauge, Gary R.		
Qy	1921	AAAAAAAGTGTATTGTCTGCTGCAATAAGTAAGTGTGACTCTGTGAC	1980			APPLICANT: Vedvick, Thomas S.		
Db	1921	AAAAAAAGTGTATTGTCTGCTGCAATAAGTAAGTGTGACTCTGTGAC	1980			APPLICANT: Carter, Darrick		
Qy	1981	CCCTTTTAATGCGTGTGATCTAAATAATGCAAGTGTAGAAACGAGGTGTCAGTC	2040			APPLICANT: Watanabe, Yoshihiro		
Db	1981	CCCTTTTAATGCGTGTGATCTAAATAATGCAAGTGTAGAAACGAGGTGTCAGTC	2040			APPLICANT: Henderson, Robert A.		
Qy	1981	TACTGCTGGCGAGGGATCATTTGAAAGCTTAAACTAAGTGTAGAAACGAGGTGTCAGTC	2100			APPLICANT: Kalos, Michael D.		
Db	1981	TACTGCTGGCGAGGGATCATTTGAAAGCTTAAACTAAGTGTAGAAACGAGGTGTCAGTC	2100			APPLICANT: Mericle, Barbara		
Qy	2041	Spies, Gregory A.				APPLICANT: Spies, Gregory A.		
Db	2041	Fan, Liqun				APPLICANT: Fan, Liqun		
Qy	2101	Wang, Tongtong				APPLICANT: Wang, Tongtong		
Db	2101	Yoshihiro				TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY		
Qy	2161	Hendereson				TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER		
Db	2161	Robert A.				FILE REFERENCE: 210121-455C18		
Qy	2221	Kalos, Michael D.				CURRENT APPLICATION NUMBER: US/10/117-982		
Db	2221	Barbara				CURRENT FILING DATE: 2002-04-15		
Qy	2281	Mericle, Barbara				CURRENT FILING DATE: 2002-04-15		
Db	2281	Spies, Gregory A.				CURRENT FILING DATE: 2002-04-15		
Qy	2341	Poy, Teresa M.				CURRENT FILING DATE: 2002-04-15		
Db	2341	Fauge, Gary R.				CURRENT FILING DATE: 2002-04-15		
Qy	2401	Vedvick, Thomas S.				CURRENT FILING DATE: 2002-04-15		
Db	2401	Carter, Darrick				CURRENT FILING DATE: 2002-04-15		
Qy	2461	Watanabe, Yoshihiro				CURRENT FILING DATE: 2002-04-15		
Db	2461	Hendereson, Robert A.				CURRENT FILING DATE: 2002-04-15		
Qy	2521	Kalos, Michael D.				CURRENT FILING DATE: 2002-04-15		
Db	2521	Barbara				CURRENT FILING DATE: 2002-04-15		
Qy	2581	Spies, Gregory A.				CURRENT FILING DATE: 2002-04-15		
Db	2581	Fan, Liqun				CURRENT FILING DATE: 2002-04-15		
Qy	2641	Wang, Tongtong				CURRENT FILING DATE: 2002-04-15		
Db	2641	Yoshihiro				CURRENT FILING DATE: 2002-04-15		
Qy	2701	Hendereson				CURRENT FILING DATE: 2002-04-15		
Db	2701	Robert A.				CURRENT FILING DATE: 2002-04-15		
Qy	2761	Kalos, Michael D.				CURRENT FILING DATE: 2002-04-15		
Db	2761	Barbara				CURRENT FILING DATE: 2002-04-15		
Qy	2816	Spies, Gregory A.				CURRENT FILING DATE: 2002-04-15		
Db	2816	Fan, Liqun				CURRENT FILING DATE: 2002-04-15		

Db	1981	CCCTTTAATGGTCATGTAATAATTGCAAGTAAGAACGAAAGGTCAAGTG 2040	US-10-393-590-26
Qy	2041	TACTGCTGGGAGCAGGGTGTCAATTACAAAAGTAATCAACTTGTGGGGAGAGTTC 2100	Sequence 26, Application US/10193590
Db	2041	TACTGCTGGGAGCAGGGTGTCAATTACAAAAGTAATCAACTTGTGGGGAGAGTTC 2100	Publication No. US20030190656A1.
Db	2101	TTTGTGAGAACTTGCATTATTGTGTCCTCCCATGTTAGTAGAACATTCCTTAAT 2160	GENERAL INFORMATION:
Qy	2101	TTTGTGAGAACTTGCATTATTGTGTCCTCCCATGTTAGTAGAACATTCCTTAAT 2160	APPLICANT: WANG, YIMIN
Db	2101	TTTGTGAGAACTTGCATTATTGTGTCCTCCCATGTTAGTAGAACATTCCTTAAT 2160	TITLE OF INVENTION: BREAST CANCER PROGNOSTIC PORTFOLIO
Qy	2161	GCTGTGTAAGAACTTGCATTATTGTGTCCTCCCATGTTAGTAGAACATTCCTTAAT 2200	FILE REFERENCE: CDS 268 US NP
Db	2161	GCTGTGTAAGAACTTGCATTATTGTGTCCTCCCATGTTAGTAGAACATTCCTTAAT 2200	CURRENT APPLICATION NUMBER: US/10/393,590
Qy	2221	CATGAAACCCTGGAAACCTACTAACAAAAAAACTGTTGGCCCCCATAGCAGGTGAA 2280	CURRENT FILING DATE: 2003-03-21
Db	2221	CATGAAACCCTGGAAACCTACTAACAAAAAAACTGTTGGCCCCCATAGCAGGTGAA 2280	PRIOR APPLICATION NUMBER: 60/168,789
Qy	2281	CTCATTGTCCTTAATAGAAAGAACAAATCCACCCAGTAAATTGCCCCTTACGTAGT 2340	PRIOR FILING DATE: 2002-03-29
Db	2281	CTCATTGTCCTTAATAGAAAGAACAAATCCACCCAGTAAATTGCCCCTTACGTAGT 2340	NUMBER OF SEQ ID NOS: 100
Db	2341	TGTTTACCTATTCAAGCTCAATAATTGAACTGCTCAGAACATTCTGTGATT 2400	SOFTWARE: PatentIn version 3.1
Qy	2341	TGTTTACCTATTCAAGCTCAATAATTGAACTGCTCAGAACATTCTGTGATT 2400	SEQ ID NO: 26
Db	2341	TGTTTACCTATTCAAGCTCAATAATTGAACTGCTCAGAACATTCTGTGATT 2400	LENGTH: 2816
Qy	2401	AATTGCTTAATTAGAGCTCTATCCCTAACCTACCCATAAAACGCCATATT 2460	TYPE: DNA
Db	2401	AATTGCTTAATTAGAGCTCTATCCCTAACCTACCCATAAAACGCCATATT 2460	ORGANISM: human
Qy	2461	CTGATACTTTCACTGGCATTTAGCCAGGAGACTAACGTTGACTAACG 2520	RESULT 6
Db	2461	CTGATACTTTCACTGGCATTTAGCCAGGAGACTAACGTTGACTAACG 2520	US-10-393-590-26
Qy	2521	AGACGTGTTAAATTAGCACTCTGGACTGGAAATTAGATGAAAGGTAGACTT 2580	Sequence 26, Application US/10193590
Db	2521	AGACGTGTTAAATTAGCACTCTGGACTGGAAATTAGATGAAAGGTAGACTT 2580	GENERAL INFORMATION:
Qy	2581	TTCTTTTTTACTCAAAGTTAACAAAGTTAGAAATCTCTGTTTCCATTAAACATAT 2640	APPLICANT: WANG, YIMIN
Db	2581	TTCTTTTTTACTCAAAGTTAACAAAGTTAGAAATCTCTGTTTCCATTAAACATAT 2640	TITLE OF INVENTION: BREAST CANCER PROGNOSTIC PORTFOLIO
Qy	2641	TTAAGATAATTAGCATAAAGACTTTAACAAAGTTAGAAATCTCTCCCATC 2700	FILE REFERENCE: CDS 268 US NP
Db	2641	TTAAGATAATTAGCATAAAGACTTTAACAAAGTTAGAAATCTCTCCCATC 2700	CURRENT APPLICATION NUMBER: US/10/393,590
Qy	2701	CACAGGACTGTGTTAAATTTCGTCAACAGCAATGTTCTGTATTGGGGTGTGTT 2760	CURRENT FILING DATE: 2003-03-21
Db	2701	CACAGGACTGTGTTAAATTTCGTCAACAGCAATGTTCTGTATTGGGGTGTGTT 2760	PRIOR APPLICATION NUMBER: 60/168,789
Qy	2761	TTGGGGATGTGATTAAATTTCATAAAACTTTGCAATTCTCGTTAAAGAAA 2816	PRIOR FILING DATE: 2002-03-29
Db	2761	TTGGGGATGTGATTAAATTTCATAAAACTTTGCAATTCTCGTTAAAGAAA 2816	NUMBER OF SEQ ID NOS: 100
Qy	721	AAAAAAGCTGAGGAGCTGCAAGGTGTCGGGGTGTGTTGGGGTGTGTTGGCGT 780	SOFTWARE: PatentIn version 3.1
Db	721	AAAAAAGCTGAGGAGCTGCAAGGTGTCGGGGTGTGTTGGGGTGTGTTGGCGT 780	SEQ ID NO: 26
Qy	781	GAATTCAAGGGGAGCATTGGCCCTCTAGTCAATTGATGAGCTGGGCAACAGC 840	LENGTH: 2816
Db	781	GAATTCAAGGGGAGCATTGGCCCTCTAGTCAATTGATGAGCTGGGCAACAGC 840	TYPE: DNA
Qy	841	CATGCCAGTATGAGATCCCATTACAGGAAAGACAGTGTGCTGTGTTACCTATGAG 900	ORGANISM: human
Db	841	CATGCCAGTATGAGATCCCATTACAGGAAAGACAGTGTGCTGTGTTACCTATGAG 900	RESULT 6
Qy	901	CCACCCAGGGTGGCACTGAATTCAAGGAGAACAGTGTGCAATTTCATGAGCTGTAACGCACT 960	US-10-393-590-26
Db	901	CCACCCAGGGTGGCACTGAATTCAAGGAGAACAGTGTGCAATTTCATGAGCTGTAACGCACT 960	Sequence 26, Application US/10193590
Qy	961	TGTGTGGGATGAAACGGCGCTCAACATTAAATCATTTGTTACTCTGAAACCAAGAGT 1020	GENERAL INFORMATION:
Db	961	TGTGTGGGATGAAACGGCGCTCAACATTAAATCATTTGTTACTCTGAAACCAAGAGT 1020	APPLICANT: WANG, YIMIN

Sequence Data and Application Details							
1021	GGCAAGTCTGGCCGACCTGCTTTGAGCCGGATCTGTGCTGCCAGGAGAGC	1080	Qy	-	TTTGAGAACTTGTGATTATTCATGTTGAGAACATTCTTAA	216.01	TTTGAGAACTTGTGATTATTCATGTTGAGAACATTCTTAA
1021	GGGAAGTCTGGCGACCTGCTTTGAGCCGGATCTGTGCTGCCAGGAGAGC	1080	Db	-	TTTGAGAACTTGTGATTATTCATGTTGAGAACATTCTTAA	216.01	TTTGAGAACTTGTGATTATTCATGTTGAGAACATTCTTAA
1081	AGGAGGCCATGAAAGATNCATCAGAAACGCAAGTTGGACAGTAGAAAGACGGT	1140	Qy	-	GCTGTGACTCCCTCTGCCACTGTATGGCATCTGTTCTCCCTCATGTAGAA	216.11	GCTGTGACTCCCTCTGCCACTGTATGGCATCTGTTCTCCCTCATGTAGAA
1081	AGGAGGCCATGAAAGATNCATCAGAAACGCAAGTTGGACAGTAGAAAGACGGT	1140	Db	-	GCTGTGACTCCCTCTGCCACTGTATGGCATCTGTTCTCCCTCATGTAGAA	216.11	GCTGTGACTCCCTCTGCCACTGTATGGCATCTGTTCTCCCTCATGTAGAA
1141	GATGTACAGGCCGGTTCTGTAGAAACACATGGTATCAGATGATCCAAAG	1200	Qy	-	CATGAAACCCGGAAAGACCTACTACAAAAAAACTGTGTTGCCCTAGGTAA	222.21	CATGAAACCCGGAAAGACCTACTACAAAAAAACTGTGTTGCCCTAGGTAA
1141	GATGTACAGGCCGGTTCTGTAGAAACACATGGTATCAGATGATCCAAAG	1200	Db	-	CATGAAACCCGGAAAGACCTACTACAAAAAAACTGTGTTGCCCTAGGTAA	222.21	CATGAAACCCGGAAAGACCTACTACAAAAAAACTGTGTTGCCCTAGGTAA
1201	AAACGAAATCTCCAGATGATGAAACTGTGTTACCTTACCACTGAGCTTAT	1260	Qy	-	CTCATTTTGTGTTTAATAGAAGAACAACTCCACCCAGTAATGCCCTTAC	228.81	CTCATTTTGTGTTTAATAGAAGAACAACTCCACCCAGTAATGCCCTTAC
1201	AAACGAAATCTCCAGATGATGAAACTGTGTTACCTTACCACTGAGCTTAT	1260	Db	-	CTCATTTTGTGTTTAATAGAAGAACAACTCCACCCAGTAATGCCCTTAC	228.81	CTCATTTTGTGTTTAATAGAAGAACAACTCCACCCAGTAATGCCCTTAC
1261	GAATGCGTGTGAGATCAAAGAGTCCCTCATGAGTACCTTCTCAGCACACA	1320	Qy	-	TGTTTACATTCAAGCTTAAAGATAAATTGAACTTCAAAATCTGTGATT	240.01	TGTTTACATTCAAGCTTAAAGATAAATTGAACTTCAAAATCTGTGATT
1261	GAATGCGTGTGAGATCAAAGAGTCCCTCATGAGTACCTTCTCAGCACACA	1320	Db	-	TGTTTACATTCAAGCTTAAAGATAAATTGAACTTCAAAATCTGTGATT	240.01	TGTTTACATTCAAGCTTAAAGATAAATTGAACTTCAAAATCTGTGATT
1321	ATGAAACGTAACGGCAACGGCAACGACGACGACGACGACTTCTGAAACATTC	1380	Qy	-	AATTGCTTAATTAGACCTCTATCCCTCAAGCTTACCTCCATAATTAA	246.61	AATTGCTTAATTAGACCTCTATCCCTCAAGCTTACCTCCATAATTAA
1321	ATGAAACGTAACGGCAACGGCAACGACGACGACGACGACTTCTGAAACATTC	1380	Db	-	AATTGCTTAATTAGACCTCTATCCCTCAAGCTTACCTCCATAATTAA	246.61	AATTGCTTAATTAGACCTCTATCCCTCAAGCTTACCTCCATAATTAA
1381	CTTTCAGCCGCTTCAGGATGAGTTGAGCCGGAGAAACTCCAAAACAACTT	1440	Qy	-	CTGATACCTGTCAGTSCATTAGCCAGGAGACTTACGTTTGTGAACTGAGC	252.21	CTGATACCTGTCAGTSCATTAGCCAGGAGACTTACGTTTGTGAACTGAGC
1381	CTTTCAGCCGCTTCAGGATGAGTTGAGCCGGAGAAACTCCAAAACAACTT	1440	Db	-	CTGATACCTGTCAGTSCATTAGCCAGGAGACTTACGTTTGTGAACTGAGC	252.21	CTGATACCTGTCAGTSCATTAGCCAGGAGACTTACGTTTGTGAACTGAGC
1441	GACGTCTTCTTTAGATCAAAGCCATTCAGTGTACCCATAGTGACGCCCTATC	1500	Qy	-	2521 AGACGPTTAAATAATCGCACTCTGGACTGGAAATTAAAGATTGAAAGGTAGACTACTT	258.21	2521 AGACGPTTAAATACTGGACTGGAAATTAAAGATTGAAAGGTAGACTACTT
1441	GACGTCTTCTTTAGATCAAAGCCATTCAGTGTACCCATAGTGACGCCCTATC	1500	Db	-	2521 AGACGPTTAAATACTGGACTGGAAATTAAAGATTGAAAGGTAGACTACTT	258.21	2521 AGACGPTTAAATACTGGACTGGAAATTAAAGATTGAAAGGTAGACTACTT
1501	TCPATATTTCAGTGTGTTGTTATTTCATGTGTTATGTGTTGTTGTTGTTA	1560	Qy	-	258.81 TTCTTTTTTACTCAAAGTTAGAGAACTCTCTGTTCTGACTGGAAATTAAACATATT	264.91	258.81 TTCTTTTTTACTCAAAGTTAGAGAACTCTCTGTTCTGACTGGAAATTAAACATATT
1501	TCPATATTTCAGTGTGTTGTTATTTCATGTGTTATGTGTTGTTGTTA	1560	Db	-	258.81 TTCTTTTTTACTCAAAGTTAGAGAACTCTCTGTTCTGACTGGAAATTAAACATATT	264.91	258.81 TTCTTTTTTACTCAAAGTTAGAGAACTCTCTGTTCTGACTGGAAATTAAACATATT
1561	TGTTGTGGTGTGTTGTTATCTAGCCCTCATAAACGGACTTAAAGCTTCAAGA	1620	Qy	-	264.61 TTAAGGATAATGCAAAACTTAAAGCTTCAACCCAGCTTCCATTCACCCAGT	270.00	264.61 TTAAGGATAATGCAAAACTTAAAGCTTCAACCCAGCTTCCATTCACCCAGT
1561	TGTTGTGGTGTGTTATCTAGCCCTCATAAACGGACTTAAAGCTTCAAGA	1620	Db	-	264.61 TTAAGGATAATGCAAAACTTAAAGCTTCAACCCAGCTTCCATTCACCCAGT	270.00	264.61 TTAAGGATAATGCAAAACTTAAAGCTTCAACCCAGCTTCCATTCACCCAGT
1621	CCCACATGCTCAAGGCCAAAGCCACTTAAAGTGGAGAACTTGTGTTGTTGTTA	1680	Qy	-	270.1 CACCAGCACTTATTCATGTGTTGTTGTTGTTGTTGTTGTTGTTGCTT	276.00	270.1 CACCAGCACTTATTCATGTGTTGTTGTTGTTGTTGTTGTTGCTT
1621	CCCACATGCTCAAGGCCAAAGCCACTTAAAGTGGAGAACTTGTGTTGTTA	1680	Db	-	270.1 CACCAGCACTTATTCATGTGTTGTTGTTGTTGTTGTTGTTGCTT	276.00	270.1 CACCAGCACTTATTCATGTGTTGTTGTTGTTGTTGTTGCTT
1681	TTACAAAGAAAGGTGTTCTGAGATTTGATCCTTAAGCCGGCCATTGTTGGTGA	1740	Qy	-	276.1 TTGTGGATGTGTTGATTAACTTCAATAAACTTTGGATCTGGTTAAAGAAA	281.6	276.1 TTGTGGATGTGTTGATTAACTTCAATAAACTTTGGATCTGGTTAAAGAAA
1681	TTACAAAGAAAGGTGTTCTGAGATTTGATCCTTAAGCCGGCCATTGTTGGTGA	1740	Db	-	276.1 TTGTGGATGTGTTGATTAACTTCAATAAACTTTGGATCTGGTTAAAGAAA	281.6	276.1 TTGTGGATGTGTTGATTAACTTCAATAAACTTTGGATCTGGTTAAAGAAA
1741	GAACCACTGTGTTGCTGAGCTTATGGAAACCCTTCTGTCTCTGTGTTTCTAA	1800	Qy	RESULT 7	US-10-393-590-27		
1741	GAACCACTGTGTTGCTGAGCTTATGGAAACCCTTCTGTCTCTGTGTTTCTAA	1800	Db		; Sequence 27, Application US/10393590		
1801	GAAGGGGATTAAGATGTTATGGAAACCCTTCTGTCTCTGTGTTTCTAA	1860	Qy		; APPLICANT: WANG, YIXIN		
1801	GAAGGGGATTAAGATGTTATGGAAACCCTTCTGTCTCTGTGTTTCTAA	1860	Db		; TITLE: BREAST CANCER PROGNOSTIC PORTFOLIO		
1861	AATTCAACGGGAAGCTTGTGAGGCTCTAAACTTAAGATGTTCTTAAAGAAA	1920	Qy		; FILE REFERENCE: CDS 268 US NP		
1861	AATTCAACGGGAAGCTTGTGAGGCTCTAAACTTAAGATGTTCTTAAAGAAA	1920	Db		; CURRENT APPLICATION NUMBER: US/10/393, 590		
1861	AATTCAACGGGAAGCTTGTGAGGCTCTAAACTTAAGATGTTCTTAAAGAAA	1920	Qy		; CURRENT FILING DATE: 2003-03-21		
1861	AATTCAACGGGAAGCTTGTGAGGCTCTAAACTTAAGATGTTCTTAAAGAAA	1920	Db		; PRIOR APPLICATION NUMBER: 60/368, 789		
1921	AAAAAGGTGTTATGGCTGATAAGTAAGTGTAGGTGACTGAGACTCAGTCAG	1980	Qy		; PRIORITY FILING DATE: 2002-03-29		
1921	AAAAAGGTGTTATGGCTGATAAGTAAGTGTAGGTGACTGAGACTCAGTCAG	1980	Db		; NUMBER OF SEQ ID NOS: 100		
1981	CCCTTTTAAATGGCTGTCATGTTAAATATTGCAACTTAGTAAAGAACGGTGTAA	2040	Qy		; SEQ ID NO 27		
1981	CCCTTTTAAATGGCTGTCATGTTAAATATTGCAACTTAGTAAAGAACGGTGTAA	2040	Db		; LENGTH: DNA		
1981	TACTGCTGGCAGGGAGGTGATCATTACCAAAAGTAATCAACTTGTGTTGGGGAGAGTC	2100	Qy		; ORGANISM: human		
2041	TACTGCTGGCAGGGAGGTGATCATTACCAAAAGTAATCAACTTGTGTTGGGGAGAGTC	2100	Qy		US-10-393-590-27		
2041	TACTGCTGGCAGGGAGGTGATCATTACCAAAAGTAATCAACTTGTGTTGGGGAGAGTC	2100	Db		Query Match 100.0%; Score 2816; DB 16;		
2041	TACTGCTGGCAGGGAGGTGATCATTACCAAAAGTAATCAACTTGTGTTGGGGAGAGTC	2100	Qy		Best Local Similarity 100.0%; Pred. No. 0;		
2041	TACTGCTGGCAGGGAGGTGATCATTACCAAAAGTAATCAACTTGTGTTGGGGAGAGTC	2100	Db		Matches 2816; Conservative 0; Mismatches 0;		
2041	TACTGCTGGCAGGGAGGTGATCATTACCAAAAGTAATCAACTTGTGTTGGGGAGAGTC	2100	Qy		Indels 0; Gaps 0;		

Db	2341	TGTTTACCATTAAGCTCAAAATAGAATTGTGAGCCCTCTCACAAAATCTGTGATT	2400		Db	241	ATTGACTTGAACTTGTGGATGAAAGCATCAGAAGTAGTGGGACAAACAGATTGAGATT	300
Qy	2401	AATTGCTTAATTAGACCTTCTACCTCCCTAACGCCCTACCTAACCTAACCCATATA	2460		Qy	301	AGCATGGACTGTGTTATCGCATGCAAGGACTCTGGACCTTGACTGACCCCCATGTGGCCCATGATC	360
Db	2401	AATTGCTTAATTAGACCTTCTACCTCCCTAACGCCCTACCTAACCCATATA	2460		Db	301	AGCATGGACTGTGTTATCGCATGCAAGGACTCTGGACCTTGACTGACCCCCATGTGGCCCATGATC	360
Qy	2461	CTGATAGTCAGTGCAGTTAGCCAGGAGACTTAGTTTGACTAAGTGAATGCCAGC	2520		Qy	361	ACGAAACCTGGGGCTCTGACAGCTGACAGCTGACAGGAGATTAGAAGGGCTCTGTGTCACC	420
Db	2461	CTGATAGTCAGTGCAGTTAGCCAGGAGACTTAGTTTGACTAAGTGAATGCCAGC	2520		Db	361	ACGAAACCTGGGGCTCTGACAGCTGACAGCTGACAGGAGATTAGAAGGGCTCTGTGTCACC	420
Qy	2521	AGACGGTGTAAATACGACACTCTGGACTGGMAATTAAAGATTGAAAGGTAGACTTT	2580		Qy	421	AGTCCTTAAACAGACGACACGGGAGAAAGGGTACGGGCCCCCTGGCCTTACGCCAG	480
Db	2521	AGACGGTGTAAATACGACACTCTGGACTGGMAATTAAAGATTGAAAGGTAGACTTT	2580		Db	421	AGTCCTTAAACAGACGACACGGGAGAAAGGGTACGGGCCCCCTGGCCTTACGCCAG	480
Qy	2581	TTCCTTTTTTACTCAAAGTTAGAGAACTCTCTGTTTCCATTAAAAAGCATATT	2640		Qy	481	CCCAGCTCCACCTTGTGATGCTCTCTCCATTACCCGCCATTCCTCCAAACGCCCTAC	540
Db	2581	TTCCTTTTTTACTCAAAGTTAGAGAACTCTCTGTTTCCATTAAAAAGCATATT	2640		Db	481	CCCAGCTCCACCTTGTGATGCTCTCTCCATTACCCGCCATTCCTCCAAACGCCCTAC	540
Qy	2641	TTAAGATAATAGCATAAAGACTTTAAATAATGTTCCCTCCCTCCATCTTCCACACCAGT	2700		Qy	541	CCAGGGCCCGAACAGTTTCAAGCTGCTTCCAGCAGTGTGACGCCAACGTCGCCACC	600
Db	2641	TTAAGATAATAGCATAAAGACTTTAAATAATGTTCCCTCCCTCCATCTTCCACACCAGT	2700		Db	541	CCAGGGCCCGAACAGTTTCAAGCTGCTTCCAGCAGTGTGACGCCAACGTCGCCACC	600
Qy	2701	CACCAAGACTGTATTTCTGTCACCAAGACATGATTCTGTATTGAGGCTGTGTT	2760		Qy	601	TGGAGTATTCCACTGAAGAACTCTACTGCAAAATTGCAAAAGCATGCCCATC	660
Db	2701	CACCAAGACTGTATTTCTGTCACCAAGACATGATTCTGTATTGAGGCTGTGTT	2760		Db	601	TGGAGTATTCCACTGAAGAACTCTACTGCAAAATTGCAAAAGCATGCCCATC	660
Qy	2761	TTGTGGATGTGATTAACTTTCAATAAACTTTGACATTTGGTTAAAGAAA	2816		Qy	661	CAGATCAAGTGTGATGCCACCTCTCACGGGAGCTTCAAGGGGCTGTATCCTGTCTAC	720
Db	2761	TTGTGGATGTGATTAACTTTCAATAAACTTTGACATTTGGTTAAAGAAA	2816		Db	661	CAGATCAAGTGTGATGCCACCTCTCACGGGAGCTTCAAGGGGCTGTATCCTGTCTAC	720
Qy	721	AAAAAAGCTGAGCACGACGTACGGAGSTGGTGAAGGGTGGGCCAACATGAGCTGAGCCGT	780		Qy	721	AAAAAAGCTGAGCACGACGTACGGAGSTGGTGAAGGGTGGGCCAACATGAGCTGAGCCGT	780
Db	721	AAAAAAGCTGAGCACGACGTACGGAGSTGGTGAAGGGTGGGCCAACATGAGCTGAGCCGT	780		Db	721	AAAAAAGCTGAGCACGACGTACGGAGSTGGTGAAGGGTGGGCCAACATGAGCTGAGCCGT	780
Qy	781	GAATTCAACCAAGGAGCAGATTGCCCTCTAGTCTTTGATTCTGAGTAGGGGAGACAGC	840		Qy	781	GAATTCAACCAAGGAGCAGATTGCCCTCTAGTCTTTGATTCTGAGTAGGGGAGACAGC	840
Db	781	GAATTCAACCAAGGAGCAGATTGCCCTCTAGTCTTTGATTCTGAGTAGGGGAGACAGC	840		Db	841	CATGCCCAAGTATGTAGAAAGATGCCATCACAGGAAGACAGATGTGTCCTGGTACCTPATGAG	900
Qy	841	CATGCCCAAGTATGTAGAAAGATGCCATCACAGGAAGACAGATGTGTCCTGGTACCTPATGAG	900		Qy	841	CATGCCCAAGTATGTAGAAAGATGCCATCACAGGAAGACAGATGTGTCCTGGTACCTPATGAG	900
Db	901	CCACCCCAGGTGTTGGGAGCTGAATTCAAGACAGTCCTGTACAATTTCATGTGTTAACAGCAGT	960		Db	901	CCACCCCAGGTGTTGGGAGCTGAATTCAAGACAGTCCTGTACAATTTCATGTGTTAACAGCAGT	960
Qy	961	TGTGTGGGGGATGAAAGATGACATGAAAGCAGCAAGTGTGCTTGGCTGGAGAGAC	1020		Qy	961	TGTGTGGGGGATGAAAGATGACATGAAAGCAGCAAGTGTGCTTGGCTGGAGAGAC	1020
Db	961	TGTGTGGGGGATGAAAGCAGCAAGTGTGCTTGGCTGGAGCTGTGCTTGGAGAGAC	1020		Db	1021	GGGCAAGTCTGGGGGATGAAAGATGACATGAAAGCAGCAAGTGTGCTTGGCTGGAGAGAC	1080
Qy	1021	GGGCAAGTCTGGGGGATGAAAGATGACATGAAAGCAGCAAGTGTGCTTGGCTGGAGAGAC	1080		Qy	1021	GGGCAAGTCTGGGGGATGAAAGATGACATGAAAGCAGCAAGTGTGCTTGGCTGGAGAGAC	1080
Db	1021	AAACCAAGATCCCAGATGAAAGATGACATGAAAGCAGCAAGTGTGCTTGGCTGGAGAGAC	1140		Db	1081	AGGAAGGGGATGAAAGATGACATGAAAGCAGCAAGTGTGCTTGGCTGGAGAGAC	1140
Qy	1081	AGGAAGGGGATGAAAGATGACATGAAAGCAGCAAGTGTGCTTGGCTGGAGAGAC	1140		Db	1081	AGGAAGGGGATGAAAGATGACATGAAAGCAGCAAGTGTGCTTGGCTGGAGAGAC	1140
Db	1141	GATGGTACAGGCGCCGTTCTGAGAACACATGGTATCCAGATGACATCCATCAAG	1200		Qy	1141	GATGGTACAGGCGCCGTTCTGAGAACACATGGTATCCAGATGACATCCATCAAG	1200
Qy	1141	GATGGTACAGGCGCCGTTCTGAGAACACATGGTATCCAGATGACATCCATCAAG	1200		Db	1141	GATGGTACAGGCGCCGTTCTGAGAACACATGGTATCCAGATGACATCCATCAAG	1200
Db	1201	AAACCAAGATCCCAGATGAAAGATGACATGAAAGCAGCAAGTGTGCTTGGCTGGAGAGAC	1260		Qy	1201	AAACCAAGATCCCAGATGAAAGATGACATGAAAGCAGCAAGTGTGCTTGGCTGGAGAGAC	1260
Qy	1201	AAACCAAGATCCCAGATGAAAGATGACATGAAAGCAGCAAGTGTGCTTGGCTGGAGAGAC	1260		Db	1261	GAATGCTGTTGAGATGAACTTACCTACAGTGGCTGGAACTCATGCAACACA	1320
Db	1261	GAATGCTGTTGAGATGAACTTACCTACAGTGGCTGGAACTCATGCAACACA	1320		Qy	1261	GAATGCTGTTGAGATGAACTTACCTACAGTGGCTGGAACTCATGCAACACA	1320
Qy	1321	ATTGAAACGTTACGGCAACAGCAACAGCAACAGCAACAGCAACAGCAACATCTC	1380		Db	1321	ATTGAAACGTTACGGCAACAGCAACAGCAACAGCAACAGCAACAGCAACATCTC	1380
Qy	1321	ATTGAAACGTTACGGCAACAGCAACAGCAACAGCAACAGCAACAGCAACATCTC	1380		Qy	1321	ATTGAAACGTTACGGCAACAGCAACAGCAACAGCAACAGCAACAGCAACATCTC	1380

RESULT 12
US-10-393-567-64

Sequence 64, Application US/10393567

PUBLICATION NO. US20030194733A1

GENERAL INFORMATION:

APPLICANT: WANG, YIXIN

TITLE OF INVENTION: CANCER DIAGNOSTIC PANEL

FILE REFERENCE: CDS 269 US NP

CURRENT APPLICATION NUMBER: US10/393,567

CURRENT FILING DATE: 2003-03-21

PRIOR APPLICATION NUMBER: 60/368,667

PRIOR FILING DATE: 2002-03-29

NUMBER OF SEQ ID NOS: 100

SOFTWARE: PatentIn version 3.1

SEQ ID NO: 64

LENGTH: 2816

TYPE: DNA

ORGANISM: human

US-10-393-567-64

Query Match 100.0% Score 2816; Length 2816;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2816; Conservative 0; Mismatches 0;
Indels 0; Gaps 0;

Query 1 TCGTGTATCAAGACAGTTGAGGAATTGAACTTCAGGTGTCACCCCT 60
Db 1 TCGTGTATCAAGACAGTTGAGGAATTGAACTTCAGGTGTCACCCCT 60
Qy 61 ACAGTACTGCCTGACCCCTACATCGGGTTCTGTAAGAACCCAGTCACTCTTG 120
Db 61 ACAGTACTGCCTGACCCCTACATCGGGTTCTGTAAGAACCCAGTCACTCTTG 120
Qy 121 AAAGAAAGTTTACCGATCCACCATGTCGAGCAACGAAATTCAATTCTCGT 180
Db 121 AAAGAAAGTTTACCGATCCACCATGTCGAGCAACGAAATTCAATTCTCGT 180
Qy 181 CCAGAGGTTTCCAGCATTCGGATTTCGGAAACACCTATATGTCAGTCAGCC 240
Db 181 CCAGAGGTTTCCAGCATTCGGATTTCGGAAACACCTATATGTCAGTCAGCC 240
Qy 241 ATGACTTGAACTTGTGATGACCATAGAAATGGTGGACAACAGATGGAT 300
Db 241 ATGACTTGAACTTGTGATGACCATAGAAATGGTGGACAACAGATGGAT 300
Qy 301 AGCATGGACTGTGATCGATGCGACTCGGACCTGACTGGACCCATGGGCCAGTC 360
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Qy 361 ACGAACCTGGGCTCCTGAAACGAGATGGACCCAGATTCAGAACGGCTCCTGTCAC 420
Db 361 ACGAACCTGGGCTCCTGAAACGAGATGGACCCAGATTCAGAACGGCTCCTGTCAC 420
Qy 421 AGTCCCTATAACAGACCAAGACAGCTCGCGAGAACAGCTCGCCCTAGGCAGA 480
Db 421 AGTCCCTATAACAGACCAAGACAGCTCGCGAGAACAGCTCGCCCTAGGCAGA 480

421 AGTCCCTATAACAGACCAAGACAGCTCGCGAGAACAGCTCGCCCTAGGCAGA 480

481 CCCAGTCACCCCTGATGCTCTCTCCATCACCCGCATCCCTCCAAACACCGACTAC 540

481 CCCAGTCACCCCTGATGCTCTCTCCATCACCCGCATCCCTCCAAACACCGACTAC 540

541 CCAGGGCGGACAGTTGACGTTGTCAGTGTGTCAGGACCCAGCCACC 600

541 CCAGGGCGGACAGTTGACGTTGTCAGTGTGTCAGGACCCAGCCACC 600

601 TGACGTTTCACTGACTGCCAAATTGCAAGACATGCCCAT 660

601 TGACGTTTCACTGACTGCCAAATTGCAAGACATGCCCAT 660

661 CAGATCAAGGTGATGCCCACTCTCAGGGAGCTGTATCGGCCATGCCCTAC 720

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841 CATGCCAGTATGAAAGATCCATCACAGGAAAGAGATGCTGCTGTTGACCTTATGAG 900

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1081 AGGAAGGGGGATGAAAGTACATCAAGAAAGGCAAGTACAGAACAGGT 1140

1081 AGGAAGGGGGATCCTGGCGACGGCGTCTGAGCTGGCTGTGCCAGAAAGAGAC 1080

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1201 AAAGAAAGATCCCAGATGAAACAGTTTACCTTACAGTCAGAAAGCAAGTCAAGAACAGCT 1260

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1321 ATTGAACGTTAGGGGACTTCAGGAAACAGGAACTCTGGGCGCTGAGACTAT 1380

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1441 GAGTCTCTTCTGATGACATTCAAGCTGACCTATGTCAGTCAGTCAGTCAGTCAGTC 1500

1501 TCTPATATTAAAGTGTGTGTGTGTGTATTCGATGTTGATATGTGAGTGTGTGTGTCA 1560

1501 TCTPATATTAAAGTGTGTGTGTGTGTATTCGATGTTGATATGTGAGTGTGTGTCA 1560

Qy	1561	TGTGTGTCGGTGTATTAGCCCTCATAAACAGGACTGAAGACACTTGGCTCAGAGA	1620	Qy	2641	TTAACATAATAGCATTAAGACTTTAAAAATGTTCCCTCCCATCTTCCCACACCCAGT	2700
Db	1561	TGTGTGTCGGTGTATTAGCCCTCATAAACAGGACTGAAGACACTTGGCTCAGAGA	1620	Db	2641	TTAACATAATAGCATTAAGACTTTAAAAATGTTCCCTCCCATCTTCCCACACCCAGT	2700
Qy	1621	CCAAACTGCTCAAGGCCAAAGGCCAAAGGCAATCTTTGAGGAGCTCAAACCT	1680	Qy	2701	CACCGGCACCTGATTTCGCTCACCAAGAACATGTTGTTGTTATTGAGCTGTT	2760
Db	1621	CCAAACTGCTCAAGGCCAAAGGCCAAAGGCCAAAGGCCAAACTGAGAACTAAACCT	1680	Db	2701	CACCGGCACCTGATTTCGCTCACCAAGAACATGTTGTTGTTATTGAGCTGTT	2760
Qy	1681	TTACAGAAAGATGTTTTCMGCAGATTSTATCCTTAAACCGGCCATGGTGTGAG	1740	Qy	2761	TTGTTGATGTTGTTATTCAATAAACCTTGACATCTTGGTTAAAAGAAA	2816
Db	1681	TTACAGAAAGATGTTTTCMGCAGATTSTATCCTTAAACCGGCCATGGTGTGAG	1740	Db	2761	TTGTTGATGTTGTTATTCAATAAACCTTGACATCTTGGTTAAAAGAAA	2816
Qy	1741	GAACCACTGCTTGTCTGAGCTTCTGTGTTCTGGAGGGGGTCAGGTGG	1800	Qy	2816	TTAACATAATAGCATTAAGACTTTAAAAATGTTCCCTCCCATCTTCCCACACCCAGT	2816
Db	1741	GAACCACTGCTTGTCTGAGCTTCTGTGTTCTGGAGGGGGTCAGGTGG	1800	Db	2816	TTAACATAATAGCATTAAGACTTTAAAAATGTTCCCTCCCATCTTCCCACACCCAGT	2816
Qy	1801	GAAGGGGCAATTAAAGTTTATGGAAACCCCTTCTGTTCTCTGTTCTAA	1860	Qy	2816	TTAACATAATAGCATTAAGACTTTAAAAATGTTCCCTCCCATCTTCCCACACCCAGT	2816
Db	1801	GAAGGGGCAATTAAAGTTTATGGAAACCCCTTCTGTTCTCTGTTCTAA	1860	Db	2816	TTAACATAATAGCATTAAGACTTTAAAAATGTTCCCTCCCATCTTCCCACACCCAGT	2816
Qy	1861	AATTCAAGGCGAAAGCTTTCAGCAGTTTCTGTTCTCTGTTCTAA	1920	Qy	2816	TTAACATAATAGCATTAAGACTTTAAAAATGTTCCCTCCCATCTTCCCACACCCAGT	2816
Db	1861	AATTCAAGGCGAAAGCTTTCAGCAGTTTCTGTTCTCTGTTCTAA	1920	Db	2816	TTAACATAATAGCATTAAGACTTTAAAAATGTTCCCTCCCATCTTCCCACACCCAGT	2816
Qy	1921	AAAAAAGTTGTTATGTCATGTCATGTCATGTCATGTCATGTCATG	1980	Qy	2816	TTAACATAATAGCATTAAGACTTTAAAAATGTTCCCTCCCATCTTCCCACACCCAGT	2816
Db	1921	AAAAAAGTTGTTATGTCATGTCATGTCATGTCATGTCATGTCATG	1980	Db	2816	TTAACATAATAGCATTAAGACTTTAAAAATGTTCCCTCCCATCTTCCCACACCCAGT	2816
Qy	1981	CCCTTTTAATGCTGGTCATGTCATGTCATGTCATGTCATGTCATG	2040	Qy	2816	TTAACATAATAGCATTAAGACTTTAAAAATGTTCCCTCCCATCTTCCCACACCCAGT	2816
Db	1981	CCCTTTTAATGCTGGTCATGTCATGTCATGTCATGTCATGTCATG	2040	Db	2816	TTAACATAATAGCATTAAGACTTTAAAAATGTTCCCTCCCATCTTCCCACACCCAGT	2816
Qy	2041	TACCTCTGGCGAGGCTTACATTACAAAGGAACTCATTTGTTGGTGGAGATTC	2100	Qy	2816	TTAACATAATAGCATTAAGACTTTAAAAATGTTCCCTCCCATCTTCCCACACCCAGT	2816
Db	2041	TACCTCTGGCGAGGCTTACATTACAAAGGAACTCATTTGTTGGTGGAGATTC	2100	Db	2816	TTAACATAATAGCATTAAGACTTTAAAAATGTTCCCTCCCATCTTCCCACACCCAGT	2816
Qy	2101	TTTGTGAGACTTGGATTATTGGTGTCTCCCTATGTTGAGACATTTCTTAT	2160	Qy	2816	TTAACATAATAGCATTAAGACTTTAAAAATGTTCCCTCCCATCTTCCCACACCCAGT	2816
Db	2101	TTTGTGAGACTTGGATTATTGGTGTCTCCCTATGTTGAGACATTTCTTAT	2160	Db	2816	TTAACATAATAGCATTAAGACTTTAAAAATGTTCCCTCCCATCTTCCCACACCCAGT	2816
Qy	2161	GCTGTGTACTGCTCTGCCACTGTGTCATCTGTTATGCTTAAGGTTTCTGTG	2220	Qy	2816	TTAACATAATAGCATTAAGACTTTAAAAATGTTCCCTCCCATCTTCCCACACCCAGT	2816
Db	2161	GCTGTGTACTGCTCTGCCACTGTGTCATCTGTTATGCTTAAGGTTTCTGTG	2220	Db	2816	TTAACATAATAGCATTAAGACTTTAAAAATGTTCCCTCCCATCTTCCCACACCCAGT	2816
Qy	2221	CATGAAACCTGGAGACCTACTGAAACAACTGTTGGTGGCCCTATGAGGTGA	2280	Qy	2816	TTAACATAATAGCATTAAGACTTTAAAAATGTTCCCTCCCATCTTCCCACACCCAGT	2816
Db	2221	CATGAAACCTGGAGACCTACTGAAACAACTGTTGGTGGCCCTATGAGGTGA	2280	Db	2816	TTAACATAATAGCATTAAGACTTTAAAAATGTTCCCTCCCATCTTCCCACACCCAGT	2816
Qy	2281	CTCATTTGGCTTTAATAGAAAGCAAACTCCCTTAATATTGGCTTACGTACT	2340	Qy	2816	TTAACATAATAGCATTAAGACTTTAAAAATGTTCCCTCCCATCTTCCCACACCCAGT	2816
Db	2281	CTCATTTGGCTTTAATAGAAAGCAAACTCCCTTAATATTGGCTTACGTACT	2340	Db	2816	TTAACATAATAGCATTAAGACTTTAAAAATGTTCCCTCCCATCTTCCCACACCCAGT	2816
Qy	2341	TGTTTACCAATTCAAGGTCAAATAAGATTGAGCCCTCTCACAAATCTGTGAT	2400	Qy	2816	TTAACATAATAGCATTAAGACTTTAAAAATGTTCCCTCCCATCTTCCCACACCCAGT	2816
Db	2341	TGTTTACCAATTCAAGGTCAAATAAGATTGAGCCCTCTCACAAATCTGTGAT	2400	Db	2816	TTAACATAATAGCATTAAGACTTTAAAAATGTTCCCTCCCATCTTCCCACACCCAGT	2816
Qy	2401	AATTGGCTTAATTAGCTTCACTTCCCTTAAGCTTCACTTCCCTAACCCATATA	2460	Qy	2816	TTAACATAATAGCATTAAGACTTTAAAAATGTTCCCTCCCATCTTCCCACACCCAGT	2816
Db	2401	AATTGGCTTAATTAGCTTCACTTCCCTAACCCATATA	2460	Db	2816	TTAACATAATAGCATTAAGACTTTAAAAATGTTCCCTCCCATCTTCCCACACCCAGT	2816
Qy	2461	CTGATACTGTTCACTTCACTTCCCTAACCCATATA	2520	Qy	2816	TTAACATAATAGCATTAAGACTTTAAAAATGTTCCCTCCCATCTTCCCACACCCAGT	2816
Db	2461	CTGATACTGTTCACTTCACTTCCCTAACCCATATA	2520	Db	2816	TTAACATAATAGCATTAAGACTTTAAAAATGTTCCCTCCCATCTTCCCACACCCAGT	2816
Qy	2521	AGACCTGTAAATAGCACTCCCTGACTGAAATAAGATTAAAGGTAGACTT	2580	Qy	2816	TTAACATAATAGCATTAAGACTTTAAAAATGTTCCCTCCCATCTTCCCACACCCAGT	2816
Db	2521	AGACCTGTAAATAGCACTCCCTGACTGAAATAAGGTAGACTT	2580	Db	2816	TTAACATAATAGCATTAAGACTTTAAAAATGTTCCCTCCCATCTTCCCACACCCAGT	2816
Qy	2581	TTCTTTTACTCAAAAGTTTACGAACTTCCTCGTTTCAATTAAACATATT	2640	Qy	2816	TTAACATAATAGCATTAAGACTTTAAAAATGTTCCCTCCCATCTTCCCACACCCAGT	2816
Db	2581	TTCTTTTACTCAAAAGTTTACGAACTTCCTCGTTTCAATTAAACATATT	2640	Db	2816	TTAACATAATAGCATTAAGACTTTAAAAATGTTCCCTCCCATCTTCCCACACCCAGT	2816

Qy	541	CCAGGCCGCCACAGTTCCACGCTTCCTTCCAGGACTCCAGAACGGCAAGTGGCCAC 600	Db	1621	CCAACTGCTCAAAGCACAAAGCCACTAGTAGAGAATCCTTGAAAGGGACTCAACCT 1680
Db	541	CCAGGCCGCCACAGTTCCACGCTTCCTTCCAGGACTCCAGAACGGCAAGTGGCCAC 600	Qy	1681	TTCAGAGAAAGGATGTGTTCTCAGATTGTTGATCTCTAGCGGCCATTGGTGGTGGAG 1740
Qy	601	TGGAGGTATTCACAAGAACTCTAATGCCAAATTGCAAGATCCCCATC 660	Db	1681	TTCAGAGAAAGGATGTGTTCTCAGATTGTTGATCTCTAGCGGCCATTGGTGGTGGAG 1740
Db	601	TGGAGGTATTCACAGAACCTACTGAAACTCTACTGCCAAATTGCAAGATCCCCATC 660	Qy	1741	GAACCACTGTGTTCTGAGGCTTCTCTGTTCTCTGGAGGGTCAAGTGGGG 1800
Qy	661	CAGTCAAAGGTGATGACCCACCTCTCAGGGAGCTGTTATGCCGCCATTCGCTGCTAC 720	Db	1741	GAACCACTGTGTTCTGAGGCTTCTCTGTTCTCTGGAGGGTCAAGTGGGG 1800
Db	661	CAGTCAAAGGTGATGACCCACCTCTCAGGGAGCTGTTATGCCGCCATTCGCTGCTAC 720	Qy	1801	GAAGGGCCTTAAGAGTGTATTGGAAACCCCTTCTGTTCTGAGGAGGGTCAAGTGGGG 1860
Qy	721	AAAAAAGCTGAGCACTGCAGGAGTGTGAGCTCCCAACCATGAGCTGAGCCGT 780	Db	1801	GAAGGGCCTTAAGAGTGTATTGGAAACCCCTTCTGTTCTGAGGAGGGTCAAGTGGGG 1860
Db	721	AAAAAAGCTGAGCACTGCAGGAGTGTGAGCTCCCAACCATGAGCTGAGCCGT 780	Qy	1861	AATTCAAGGGAGGCTTGGCAGGCTCTCAAACTTAAGATCTCTTAAAGAAAGGAG 1920
Qy	781	GAATTCAAGGAGACAGATTGCTCCCTCTAGCTGATTGAGTAGGGGAAACAG 840	Db	1861	AATTCAAGGGAGGCTTGGCAGGCTCTCAAACTTAAGATCTCTTAAAGAAAGGAG 1920
Db	781	GAATTCAAGGAGACAGATTGCTCCCTCTAGCTGAGGAGCTGTTATGGGAAACAG 840	Qy	1921	AAAAGAAGTTGTATTGCTGTTGCTGTTGAGTAAGTGTAGGAGACTCAGTCAGAGA 1980
Qy	841	CATGCCCACTATGTAAGAACATCCCATCAGGGAGTGTGTTACCTTATGAG 900	Db	1921	AAAAGAAGTTGTATTGCTGTTGCTGTTGAGTAAGTGTAGGAGACTCAGTCAGAGA 1980
Db	841	CATGCCCACTATGTAAGAACATCCCATCAGGGAGTGTGTTACCTTATGAG 900	Qy	1981	CCCTTTTAATGCTGTTGCTGTTAATAATTCGAAAGTAGTAGTAACAAAGGAGGTCAACTG 2040
Qy	901	CCACCCCAAGTTGGCACAGTCTGGAAATTCAGCAAGTGTGTTAACAGGAGT 960	Db	1981	CCCTTTTAATGCTGTTGCTGTTAATAATTCGAAAGTAGTAGTAACAAAGGAGGTCAACTG 2040
Db	901	CCACCCCAAGTTGGCACAGTCTGGAAATTCAGCAAGTGTGTTAACAGGAGT 960	Qy	2041	TACTGCTGGGAGGGAGGCTGTCATACCAAAAGTAATCAACTTCTGGGTTGAGAGTTC 2100
Qy	961	TGTTGTTGGGGATGAAACGGCGTCAATTAACTATTGTAACAGGAGAT 1020	Db	2041	TACTGCTGGGAGGGAGGCTGTCATACCAAAAGTAATCAACTTCTGGGTTGAGAGTTC 2100
Db	961	TGTTGTTGGGGATGAAACGGCGTCAATTAACTATTGTAACAGGAGAT 1020	Qy	2101	TTTGTGAGAACTTGTGATTGTCCTCCCTCATGTGTTAGTAGCAACATTCTTAAT 2160
Qy	1021	GGGCAAGTCTGGGCCAGGCTGGCTGGTCTCTGGCAGGAAGAGAC 1080	Db	2101	TTTGTGAGAACTTGTGATTGTCCTCCCTCATGTGTTAGTAGCAACATTCTTAAT 2160
Db	1021	GGGCAAGTCTGGGCCAGGCTGGCTGGTCTCTGGCAGGAAGAGAC 1080	Qy	2161	GCTGTTGTTACCTCCCTCTGCCACTGTGTTGCACTGTGTTAGCTGTTAGTGTAAAGTTTCTGTGA 2220
Qy	1081	AGGAAAGGGCGATGAGATGAGATGAGATGAGATGAGATGAGATGAGT 1140	Db	2161	GCTGTTGTTACCTCCCTCTGCCACTGTGTTGCACTGTGTTAGTGTAAAGTTTCTGTGA 2220
Db	1081	AGGAAAGGGCGATGAGATGAGATGAGATGAGATGAGATGAGATGAGT 1140	Qy	2221	CATGAACCCCTGGAAAGGACCTACTACAAAGGAAACTTGTGTTGGCCCTCATCAGGTGAA 2280
Qy	1141	GANGGTACAGGCCCGTTCTGTCAGAACACATGGTATCCAGATCACCCATCAAG 1200	Db	2221	CATGAACCCCTGGAAAGGACCTACTACAAAGGAAACTTGTGTTGGCCCTCATCAGGTGAA 2280
Db	1141	GATGGTACAGGCCCGTTCTGTCAGAACACATGGTATCCAGATCACCCATCAAG 1200	Qy	2281	CTCATTTGTGCTTTATAGAAAGAACAAATCCACCCAGTAATATGCGCTTACGTGAGT 2340
Qy	1201	AAAGGAAGATGCCAGATGAGACTGTATACTTACAGTGTAGGGGGCTGAGACTT 1260	Db	2281	CTCATTTGTGCTTTATAGAAAGAACAAATCCACCCAGTAATATGCGCTTACGTGAGT 2340
Db	1201	AAAGGAAGATGCCAGATGAGACTGTATACTTACAGTGTAGGGGGCTGAGACTT 1260	Qy	2341	TGTTTACATTATCAAGGTCAAATAGAACTTGTGTTAGCTGTTAGTGTAAAGTTCTGTGATT 2400
Qy	1261	GAATGTGTTGGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1320	Db	2341	TGTTTACATTATCAAGGTCAAATAGAACTTGTGTTAGCTGTTAGTGTAAAGTTCTGTGATT 2400
Db	1261	GAATGTGTTGGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 1320	Qy	2401	AATTGGTTAATTTAGGGCTTCTACCTACCAAAACCCCATTTA 2460
Qy	1321	ATGGAACCCAGCAAGGCAACAGGCAACAGGCAACAGGCAACAGCCTCTC 1380	Db	2401	AATTGGTTAATTTAGGGCTTCTACCTACCAAAACCCCATTTA 2460
Db	1321	ATGGAACCCAGCAAGGCAACAGGCAACAGGCAACAGGCAACAGCCTCTC 1380	Qy	2461	CTGATACGTGTTACGTCATTAGCCAGGAGACTTGTGTTAGTGTAGTCAGTCAGC 2520
Qy	1381	CTTTCAGGCTGCTGTTAGGATGAGCTGGCTGGCCGGAGAAACCTCRAAACATCT 1440	Db	2461	CTGATACGTGTTACGTCATTAGCCAGGACTTGTGTTAGTGTAGTCAGTCAGC 2520
Db	1381	CTTTCAGGCTGCTGTTAGGATGAGCTGGCTGGCCGGAGAAACCTCRAAACATCT 1440	Qy	2521	AGACGGTTAAATTCGCACTCTGACTGAAATTAAAGTTGAAGGGTAGACTTCT 2580
Qy	1441	GACGTCTCTTAACTGACATTCCAAGGCTTCAAGGCTTCAAGGCCCTATC 1500	Db	2521	AGACGGTTAAATTCGCACTCTGACTGAAATTAAAGTTGAAGGGTAGACTTCT 2580
Db	1441	GACGTCTCTTAACTGACATTCCAAGGCTTCAAGGCTTCAAGGCCCTATC 1500	Qy	2581	TCTCTTAACTGACATTCCAAGGCTTCAAGGCCCTATC 2580
Qy	1501	TCTATATTTAACTGTCGTTGTTGTTATCTGCTGACTGCTGCTGCTGCTA 1560	Db	2581	TCTCTTAACTGACATTCCAAGGCTTCAAGGCCCTATC 2580
Db	1501	TCTATATTTAACTGTCGTTGTTGTTATCTGCTGACTGCTGCTGCTGCTA 1560	Qy	2641	TAAAGATAATGCAAAACTTAAATGTTCACTTCCACACCCAGT 2700
Qy	1561	TGTTGTTGCGGTGTTATCTAGGCTCTATAAACAGGACTTGTGAGAGAACTTGTGCTCAGAGA 1620	Db	2641	TGTTGTTGCGGTGTTATCTAGGCTCTATAAACAGGACTTGTGAGAGAACTTGTGCTCAGAGA 1620
Qy	1621	CCAAACTGCTCAAAAGGCCACTAGTGTGAGAGAACTTGTGAGAGAACTTGTGCTCAGAGA 1680	Qy	2701	CACCGAACCTGCTCAAAAGGCCACTAGTGTGAGAGAACTTGTGAGAGAACTTGTGCTCAGAGA 1680

QY 1741 GAACCACTGTGTTGTCAGGCTTCTGAGCTTCTGTTGGAGGGAGGGTCAGGTGGG 1800
 Db 1741 GAACCACTGTGTTGTCAGGCTTCTGAGCTTCTGTTGGAGGGAGGGTCAGGTGGG 1800
 ; Sequence 27, Application US/10394087
 ; Publication No. US20030194734A1
 ; APPLICANT: Jatko, Tim
 ; TITLE OF INVENTION: SELECTION OF MARKERS
 ; FILE PREFERENCE: CDS 265 US NP
 ; CURRENT APPLICATION NUMBER: US/10/394,087
 ; CURRENT FILING DATE: 2003-03-21
 ; PRIOR APPLICATION NUMBER: 60/368,790
 ; PRIOR FILING DATE: 2002-03-29
 ; NUMBER OF SEQ ID NOS: 100
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 27
 ; LENGTH: 2816
 ; TYPE: DNA
 ; ORGANISM: human
 ; US-10-394-087-27

Qy 1741 AAAAAAGTTGTTATTGCTGTGCAATAACTAAGTTGAGGTGACTGAGACTGAGA 1980
 Db 1741 AAAAAGTTGTTATTGCTGTGCAATAACTAAGTTGAGGTGACTGAGACTGAGA 1980
 ; Query Match 100 %; Score 2816; DB 16; Length 2816;
 ; Best Local Similarity 100 %; Pred. No. 0;
 ; Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1741 TCGTTTATCAAAGCAGTTGAAGGAAATGAAATTGAAACTTCAGGTGTCGCCACCT 60
 Db 1741 TCGTTTATCAAAGCAGTTGAAGGAAATGAAATTGAAACTTCAGGTGTCGCCACCT 60
 ; Query Match 100 %; Score 2816; DB 16; Length 2816;
 ; Best Local Similarity 100 %; Pred. No. 0;
 ; Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1741 AGAGTACTGCCCTGACCCCTAACATCCAGCGTTCTGAGAAACCACGCTCATTTCTTGG 120
 Db 1741 AGAGTACTGCCCTGACCCCTAACATCCAGCGTTCTGAGAAACCACGCTCATTTCTTGG 120
 ; Query Match 100 %; Score 2816; DB 16; Length 2816;
 ; Best Local Similarity 100 %; Pred. No. 0;
 ; Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1741 AAAGAAAGTTTACCGATTCACCATGGCTCCCTCAGTGTAGTGAACATTTCTTAAT 2160
 Db 1741 AAAGAAAGTTTACCGATTCACCATGGCTCCCTCAGTGTAGTGAACATTTCTTAAT 2160
 ; Query Match 100 %; Score 2816; DB 16; Length 2816;
 ; Best Local Similarity 100 %; Pred. No. 0;
 ; Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1741 CGCTGTACTGCTCTGCACCTGTATCTGGCATATCTGTATGCTAAAGTTTCTCTGTA 2220
 Db 1741 CGCTGTACTGCTCTGCACCTGTATCTGGCATATCTGTATGCTAAAGTTTCTCTGTA 2220
 ; Query Match 100 %; Score 2816; DB 16; Length 2816;
 ; Best Local Similarity 100 %; Pred. No. 0;
 ; Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1741 CATGAAACCTGGAGAACCTACTACAAAAAAACTGTGTTGGCCCTCATAGCGTGA 2280
 Db 1741 CATGAAACCTGGAGAACCTACTACAAAAAAACTGTGTTGGCCCTCATAGCGTGA 2280
 ; Query Match 100 %; Score 2816; DB 16; Length 2816;
 ; Best Local Similarity 100 %; Pred. No. 0;
 ; Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1741 CTATTTGTGCTTTAATAGAAAAGAACATCCCCAGTAAATGCCCTTAGTAGT 2340
 Db 1741 CTATTTGTGCTTTAATAGAAAAGAACATCCCCAGTAAATGCCCTTAGTAGT 2340
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 ; Best Local Similarity 100 %; Pred. No. 0;
 ; Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1741 TGTTTACCATTTACAAGCTCAAATAGAAATTGAAAGCCCTCTCACAAATCTGTGAT 2400
 Db 1741 TGTTTACCATTTACAAGCTCAAATAGAAATTGAAAGCCCTCTCACAAATCTGTGAT 2400
 ; Query Match 100 %; Score 2816; DB 16; Length 2816;
 ; Best Local Similarity 100 %; Pred. No. 0;
 ; Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1741 AATTGCTTAAATTAGACGTTCTATCCCTCAAGCCTACCTACCAAAACGCCATTTA 2460
 Db 1741 AATTGCTTAAATTAGACGTTCTATCCCTCAAGCCTACCTACCAAAACGCCATTTA 2460
 ; Query Match 100 %; Score 2816; DB 16; Length 2816;
 ; Best Local Similarity 100 %; Pred. No. 0;
 ; Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1741 CTGATACGTTCAAGTCAAGCTCTGGACTGAAATTAGATTGAGCTACTACTT 2520
 Db 1741 CTGATACGTTCAAGTCAAGCTCTGGACTGAAATTAGATTGAGCTACTACTT 2520
 ; Query Match 100 %; Score 2816; DB 16; Length 2816;
 ; Best Local Similarity 100 %; Pred. No. 0;
 ; Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1741 AGACGTGTTAAATCTGGACTGAAATTAGATTGAAAGGTAGCTACTT 2580
 Db 1741 AGACGTGTTAAATCTGGACTGAAATTAGATTGAAAGGTAGCTACTT 2580
 ; Query Match 100 %; Score 2816; DB 16; Length 2816;
 ; Best Local Similarity 100 %; Pred. No. 0;
 ; Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1741 TCTCTTTTCTTACTCAAAAGTTAGAGATACTCTCTCCATTTAAACACATTT 2640
 Db 1741 TCTCTTTTCTTACTCAAAAGTTAGAGATACTCTCTCCATTTAAACACATTT 2640
 ; Query Match 100 %; Score 2816; DB 16; Length 2816;
 ; Best Local Similarity 100 %; Pred. No. 0;
 ; Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1741 TTAGATATAAGCTTAAGACTTAAATTGTTAGAGATCTCTCTCCACCCATT 2700
 Db 1741 TTAGATATAAGCTTAAGACTTAAATTGTTAGAGATCTCTCTCCACCCATT 2700
 ; Query Match 100 %; Score 2816; DB 16; Length 2816;
 ; Best Local Similarity 100 %; Pred. No. 0;
 ; Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1741 CACCAAGCTGTTATTCTGTCACCAAGAACATGATTCTGTTATTGAGGTGTTGCTT 2760
 Db 1741 CACCAAGCTGTTATTCTGTCACCAAGAACATGATTCTGTTATTGAGGTGTTGCTT 2760
 ; Query Match 100 %; Score 2816; DB 16; Length 2816;
 ; Best Local Similarity 100 %; Pred. No. 0;
 ; Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1741 TTCTGGATGTTGCTATTAAATTCTCAATAAACTTCTGCTTAAAGAAA 2816
 Db 1741 TTCTGGATGTTGCTATTAAATTCTCAATAAACTTCTGCTTAAAGAAA 2816
 ; Query Match 100 %; Score 2816; DB 16; Length 2816;
 ; Best Local Similarity 100 %; Pred. No. 0;
 ; Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1741 CAGATCAAGGTGATGACCCCACTCTCTGAGAGACATGCTCTTCTGCTAC 2880
 Db 1741 CAGATCAAGGTGATGACCCCACTCTCTGAGAGACATGCTCTTCTGCTAC 2880
 ; Query Match 100 %; Score 2816; DB 16; Length 2816;
 ; Best Local Similarity 100 %; Pred. No. 0;
 ; Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1741 CCCAGCTCCACCTTCATGCTCTCTCCATCAGGACCTCTCCCTCAACCCGACTAC 360
 Db 1741 CCCAGCTCCACCTTCATGCTCTCTCCATCAGGACCTCTCCCTCAACCCGACTAC 360
 ; Query Match 100 %; Score 2816; DB 16; Length 2816;
 ; Best Local Similarity 100 %; Pred. No. 0;
 ; Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1741 AGGAACCTGGGGCTCTCTGGATGCTCTCTGGAAACGGCATTTCTGTCGCCACC 420
 Db 1741 AGGAACCTGGGGCTCTCTGGATGCTCTCTGGAAACGGCATTTCTGTCGCCACC 420
 ; Query Match 100 %; Score 2816; DB 16; Length 2816;
 ; Best Local Similarity 100 %; Pred. No. 0;
 ; Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1741 AGTCCCTATAACACAGAACAGGCTAACAGCTGTAACGGGGCCCTGCCTCTAGGACAG 480
 Db 1741 AGTCCCTATAACACAGAACAGGCTAACAGCTGTAACGGGGCCCTGCCTCTAGGACAG 480
 ; Query Match 100 %; Score 2816; DB 16; Length 2816;
 ; Best Local Similarity 100 %; Pred. No. 0;
 ; Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1741 CCCAGCTCCACCTTCATGCTCTCTCCATCAGGACCTCTCCCTCAACCCGACTAC 540
 Db 1741 CCCAGCTCCACCTTCATGCTCTCTCCATCAGGACCTCTCCCTCAACCCGACTAC 540
 ; Query Match 100 %; Score 2816; DB 16; Length 2816;
 ; Best Local Similarity 100 %; Pred. No. 0;
 ; Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1741 CCAGGGCCGACAGTTTCGAGGTGCTCTCCATCAGGACCTCTCCCTCAACCCGACTAC 600
 Db 1741 CCAGGGCCGACAGTTTCGAGGTGCTCTCCATCAGGACCTCTCCCTCAACCCGACTAC 600
 ; Query Match 100 %; Score 2816; DB 16; Length 2816;
 ; Best Local Similarity 100 %; Pred. No. 0;
 ; Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1741 TTGACCTTATTCTGACAACTGAAATTGTTATTGAGCTACTGCTTAAAGACTCTGCTAC 720
 Db 1741 TTGACCTTATTCTGACAACTGAAATTGTTATTGAGCTACTGCTTAAAGACTCTGCTAC 720
 ; Query Match 100 %; Score 2816; DB 16; Length 2816;
 ; Best Local Similarity 100 %; Pred. No. 0;
 ; Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1741 CAGATCAAGGTGATGACCCCACTCTCTGAGAGACATGCTCTTCTGCTAC 720
 Db 1741 CAGATCAAGGTGATGACCCCACTCTCTGAGAGACATGCTCTTCTGCTAC 720
 ; Query Match 100 %; Score 2816; DB 16; Length 2816;
 ; Best Local Similarity 100 %; Pred. No. 0;
 ; Matches 2816; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	721	AAAAAAGCTGACGACSTCACGGAGGTTGTAAGCGTGCACCTGACTGACCGT	780
Db	721	AAAAAAGCTGACGACSTCACGGAGGTTGTAAGCGTGCACCTGACTGACCGT	780
Qy	781	GAATTCACGAGGGACAGATGCCCTCCTAGTCATTGATTGAGTAAAGGGAACGC	840
Db	781	GAATTCACGAGGGACAGATGCCCTCCTAGTCATTGATTGAGTAAAGGGAACGC	840
Qy	841	CATGCCCATATGTGACAAGATCCCATCACAGGAAGACAGAGTGCTGACCTTATGAG	900
Db	841	CATGCCCATATGTGACAAGATCCCATCACAGGAAGACAGAGTGCTGACCTTATGAG	900
Qy	901	CCACCCCCAGGGTTGCACTGATTCAAGACAGCTCTGTTACATTGTTACCTGTAACCGAGT	960
Db	901	CCACCCCCAGGGTTGCACTGATTCAAGACAGCTCTGTTACATTGTTACCTGTAACCGAGT	960
Qy	961	TGTGTTGGAGGGATGAAACGGCCTCAATTAACTTGTGAAACAGAGAT	1020
Db	961	TGTGTTGGAGGGATGAAACGGCCTCAATTAACTTGTGAAACAGAGAT	1020
Qy	1021	GGCCCAAGTCTGGGGCGACCTGCTGTTGAGGCCGGATCTGTGCTGCCAGGAAGAC	1080
Db	1021	GGCCCAAGTCTGGGGCGACCTGCTGTTGAGGCCGGATCTGTGCTGCCAGGAAGAC	1080
Qy	1081	AGGAGGGCATGAGATACTGATCATCGAACAGCAAGCTTGGACAGTAAAGACGGT	1140
Db	1081	AGGAGGGCATGAGATACTGATCATCGAACAGCAAGCTTGGACAGTAAAGACGGT	1140
Qy	1141	GATGGTAGAACAGGCGCCGTTTCGTCAGAACACATGGTAACTCCATCAAG	1200
Db	1141	GATGGTAGAACAGGCGCCGTTTCGTCAGAACACATGGTAACTCCATCAAG	1200
Qy	1201	AAACGAAAGATCCCCAGATGAACTGTATACTTACCACTGAGCTGCTGAGACTTAT	1260
Db	1201	AAACGAAAGATCCCCAGATGAACTGTATACTTACCACTGAGCTGCTGAGACTTAT	1260
Qy	1261	GAAATGCTGTGAGATAAGAGTCAAGAGTCCCTGGAAACTCATGGAGTACCTCTCAGCA	1320
Db	1261	GAAATGCTGTGAGATAAGAGTCAAGAGTCCCTGGAAACTCATGGAGTACCTCTCAGCA	1320
Qy	1321	ATGAAACGTAACGGCAACGGCAAACGGAGGAACTCCAAAACATCT	1380
Db	1321	ATGAAACGTAACGGCAACGGCAAACGGAGGAACTCCAAAACATCT	1380
Qy	1381	CITTCAGCCCTGCTTCAGGAATGAGCTTGTGAGGCCGGAGAGAAACTCCAAAACATCT	1440
Db	1381	CITTCAGCCCTGCTTCAGGAATGAGCTTGTGAGGCCGGAGAGAAACTCCAAAACATCT	1440
Qy	1441	GACGTCTCTTGTGACATTGACATCGACCCCAACCATCAGTGACCTGACGCCCTATC	1500
Db	1441	GACGTCTCTTGTGACATTGACATCGACCCCAACCATCAGTGACCTGACGCCCTATC	1500
Qy	1501	TCTATATTTAAGTGTGTGTATTTCGATGTGTTAAAGTGTGTTGTTGTTGTA	1560
Db	1501	TCTATATTTAAGTGTGTGTATTTCGATGTGTTAAAGTGTGTTGTTGTTGTA	1560
Qy	1561	TGTGTTGCTGTGTTGTTGCTATCGCCCTCATAAACAGGAACTTGAGACACTTGTGCTCAGAGA	1620
Db	1561	TGTGTTGCTGTGTTGCTATCGCCCTCATAAACAGGAACTTGAGACACTTGTGCTCAGAGA	1620
Qy	1681	TTACAGAAAGGATTTCTCGCAGATTGTTGATCTTACGCGGCCATTGGTGGTGA	1740
Db	1681	TTACAGAAAGGATTTCTCGCAGATTGTTGATCTTACGCGGCCATTGGTGGTGA	1740
Qy	1741	GAACCACTGCTCAAAGGCCAACTAGTGAGAAATCTTGTGAGGGAACCAACCT	1800
Db	1741	GAACCACTGCTCAAAGGCCAACTAGTGAGAAATCTTGTGAGGGAACCAACCT	1800
Qy	1741	GAACCACTGCTCAAAGGCCAACTAGTGAGAAATCTTGTGAGGGAACCAACCT	1800
Db	1741	GAACCACTGCTCAAAGGCCAACTAGTGAGAAATCTTGTGAGGGAACCAACCT	1800

Search completed: October 3, 2005, 14:01:42

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 3, 2005, 06:01:58 ; Search time 247 Seconds (without alignments)

Perfect score: 2383

Title: US-09-670-568C-1

Sequence: 1 MSQSTQTNEFLSPEVQHQIWW.....PKQSDVFVFRHSKPNNRSVYP 448

Scoring table: BLOSUM62

Xgapop	10.0	Xgapext	0.5
Ygapop	10.0	Ygapext	0.5
Fgapop	6.0	Fgapext	7.0
Delop	6.0	Delext	7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Qr -cgn2_1/USP0670566/runat_03102005_070150_24303/app/query.fasta_1.647
-DB=Issued_Patents_NA -QEMT=Fastmt -SUFFIXxrn -MINNATCH=0.1 -LOOPCL=0
-LOOPENT=0 -UNITS=Bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40_cdi
-LIST=ALIGN -THR SCORE=pct -THR MIN=0 -THR MAX=100 -ALIGN=15
-MODE=LOCAL -OUTEMT=pct -NORM=ext -HEAPSIZT=500 -MINLEN=0 -MAXLEN=1000000000
-USER=US09670568 @CGN 1.1.177 @runat_03102005_070150_24303 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT_DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Database : Issued Patents NA:
1: /cgn2_6/p2odata/1/ina/IA_COMB.seq:*
2: /cgn2_6/p2odata/1/ina/IB_COMB.seq:*
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4: /cgn2_6/p2odata/1/ina/6B_COMB.seq:*
5: /cgn2_6/p2odata/1/ina/ACTUS_COMB.seq:*
6: /cgn2_6/p2odata/1/ina/backfiles.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULTS

Result No.	Score	Query Match Length	DB ID	Description
1	2383	100.0	2810 4	US-09-949-016-5447 Sequence 5447, App
2	2383	100.0	2816 3	US-09-643-597-333 Sequence 333, App
3	2383	100.0	2816 4	US-09-542-615A-333 Sequence 333, App
4	2383	100.0	2816 4	US-09-606-421B-333 Sequence 333, App
5	2383	100.0	2816 4	US-09-630-940B-333 Sequence 333, App
6	2185	91.7	1551 3	US-09-643-597-337 Sequence 337, App
7	2185	91.7	1551 4	US-09-606-421B-337 Sequence 337, App
8	2185	91.7	1551 4	US-09-630-940B-337 Sequence 337, App
9	2185	91.7	1551 4	US-09-630-940B-337 Sequence 337, App
10	2185	91.7	2270 3	US-09-643-597-332 Sequence 332, App
11	2185	91.7	2270 4	US-09-542-615A-332 Sequence 332, App
12	2185	91.7	2270 4	US-09-606-421B-332 Sequence 332, App

ALIGNMENTS

Result	Score	Query Match Length	DB ID	Description
1	2383	100.0	2810 4	US-09-949-016-5447 Sequence 5447, App
2	2383	100.0	2816 3	US-09-643-597-333 Sequence 333, App
3	2383	100.0	2816 4	US-09-542-615A-333 Sequence 333, App
4	2383	100.0	2816 4	US-09-606-421B-333 Sequence 333, App
5	2383	100.0	2816 4	US-09-630-940B-333 Sequence 333, App
6	2185	91.7	1551 3	US-09-643-597-337 Sequence 337, App
7	2185	91.7	1551 4	US-09-606-421B-337 Sequence 337, App
8	2185	91.7	1551 4	US-09-630-940B-337 Sequence 337, App
9	2185	91.7	1551 4	US-09-630-940B-337 Sequence 337, App
10	2185	91.7	2270 3	US-09-643-597-332 Sequence 332, App
11	2185	91.7	2270 4	US-09-542-615A-332 Sequence 332, App
12	2185	91.7	2270 4	US-09-606-421B-332 Sequence 332, App

RESULTS

Result	Score	Query Match Length	DB ID	Description
1	2383	100.0	2810 4	US-09-949-016-5447 Sequence 5447, App
2	2383	100.0	2816 3	US-09-643-597-333 Sequence 333, App
3	2383	100.0	2816 4	US-09-542-615A-333 Sequence 333, App
4	2383	100.0	2816 4	US-09-606-421B-333 Sequence 333, App
5	2383	100.0	2816 4	US-09-630-940B-333 Sequence 333, App
6	2185	91.7	1551 3	US-09-643-597-337 Sequence 337, App
7	2185	91.7	1551 4	US-09-606-421B-337 Sequence 337, App
8	2185	91.7	1551 4	US-09-630-940B-337 Sequence 337, App
9	2185	91.7	1551 4	US-09-630-940B-337 Sequence 337, App
10	2185	91.7	2270 3	US-09-643-597-332 Sequence 332, App
11	2185	91.7	2270 4	US-09-542-615A-332 Sequence 332, App
12	2185	91.7	2270 4	US-09-606-421B-332 Sequence 332, App

Length: 2810
Matches: 448
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-09-670-568C-1 (1-448) x US-09-949-016-5447 (1-2810)
Qy 1 MetSerGinSerThrGlnThrAsnGluHeLeuserProGluValPheGlnHistileTrp 20

Qy	1 MetAspGlnGlnIleGlnAsnGlySerSerThrSerProTyroAsnThrAspHisAla 100	Db	1465 cccCAACCGATCTAGTGTACCC 1488
Db	385 ATGGACCAAGCAGATTCAAGAACGGCTCCCTGTCACCCGCTATAACAGACCCCG 444		
Qy	101 GlnAsnSerValThrAlaProSerProTyraGlnProSerSerThrPheAspAla 120		
Db	445 CGAAACAGCTACGGCCCTGCCCTACGACAGCCAGTCACCTTGATGCTC 504		
Qy	121 SerProSerProAlaLeProSerProTyroProHisSerPheAspVal 140		
Db	505 TCTCCATACCGCCATCCCTCAAGCCGACTACCCAGGCCAGTCAGTTGAGTG 564		
Qy	141 SerPheGlnGlnSerSerThrAlaLysSerThrSerThrGluLeuLys 160		
Db	565 TCCTTCCAAGCAGTCAGCACCCGCAACTGGCACCTTGACCTATTCACGTGAG 624		
Qy	161 LysLeuTyrcysGlnIleAlaLysThrCysProLeuGlnIleLysValMetThrProPro 180		
Db	625 AAATCTACTGCAAATTGAAAGCATGCCCATCAGATAAGGTGATGACCCACT 684		
Qy	181 ProGlnGlyAlaValLeuArgAlaMetProValTyrosLysAlaGluHisValThrGlu 200		
Db	685 CCTCAGGGAGCTGTTATCGCCCATCTGTCATAAAAAGCTGACACTCACGGAG 744		
Qy	201 ValAlaValLeuArgAlaMetProValTyrosLysAlaGluGlnIleAla 220		
Db	745 GTGGTGAAGCGTGGTCCCACCATGAGCTGAATCACGGGACAGATTGCC 804		
Qy	221 ProProSerHisLeuIleArgValGluGlyAsnGluGlyGlnIleAla 240		
Db	805 CCTCCTAGTCATTGATGAGTAGAGGGACAGCATGCCAGATGAGAGATGCC 864		
Qy	241 IleThrGlyArgGlnValProProGlnValGlyThrGluPhe 260		
Db	865 ATCACAGGAAGCAGACTGTGCTGACTCTATGAGCAACCCCAAGGGACTGAACT 924		
Qy	261 ThrThrValLeuTyrAsnPhenMetCysAsnSerSerCysValGlyIleAsnArg 280		
Db	925 ACGACACTCTGTACAATTTCATGTGTAACACCGAGTTGGAGGTGACCCGGT 984		
Qy	281 ProlleuIleLeuValThrLeuGluThrArgAspGlyGlnValLeuGlyArgA99CYS 300		
Db	985 CCAATTTTAATCTGTACTCTGGAAACCAGAGATGGCAAGTCCGGGACCTGC 1044		
Qy	301 PheGluAlaArgGlyCysAlaCysProGlyArgAspArgLysValAspSerIle 320		
Db	1045 TTGAGGCCCGATCTGCTGCCAGAAAGCAGAAAGCAGGAAGCAG 1104		
Qy	321 ArgLyS61GlnValSerAspSerThrLysArgGlyIleAspProPheArg 340		
Db	1105 AGAAAGGAGCAAGTTCGACAGACTACAAGAACGGTGTGGATGAA 1164		
Qy	341 GlnAsnThrHisGlyIleGlnMetThrSerIleLysIleGlnSerProIleAspGlu 360		
Db	1165 CAGAACACACATGTATCAGATGAGCTTACGACATCCATAGAAAGGAGATGAA 1224		
Qy	361 LeuLeuTyrlLeuProValArgGlyIleGluThrTyrGluMetLeuLeuLysIleLysGlu 380		
Db	1225 CTGTTATCTTACCAAGTGAGGCCGGTGAACATTAATGCTGTTGAAAGTCAAGAG 1284		
Qy	381 SerLeuIleMetGlnTyrlLeuProGlnHsThrIleGluThrTyrArgGlnGln 400		
Db	1285 TCCCTGCGAACTCATGCACTACCTTCCTCAAGCACACATTGAAACGCAACACCAA 1344		
Qy	401 GlnGlnGlnHsIleLeuGlnLysIleLeuSerAlaCysPheArgAspGlu 420		
Db	1345 CAGCAGGCCAGCACTTACTTCAGAACATCTCCCTCAAGCACACATTGAAACGCAAC 1404		
Qy	421 LeuValGluProArgArgGluThrProlyGinSerAspValPhePheAspHisSerLys 440		
Db	1405 CTTGTGGAGGCCGGAGAAACTCCAAAACATCTCGCTTCCTAGATCAG 1464		
Qy	441 ProProAsnArgSerValTyrrPro 448		

Qy 181 ProGlnGlyAlaValIleArgAlaMetProValTyrLysBalaGluHisValThrGlu 200
 Db 695 CCTGGAGCCGCTTATGCCGCTTACAAAGCTGCTACAAAGCTGCCCAGTCACGGAG 744
 Qy 201 ValValLysArgCysProAsnHisGluLeuSerArgGluPheAsnGluGlyInleAla 220
 Db 745 GTCGTGAAGGGGCCAACCATGAGTGCGTGAAATTCAACAGGGAAAGATGCC 804
 Qy 221 ProProSerHisSeuIleArgValGluGlyAsnSerHisAlaGlnTrpValGluAspPro 240
 Db 805 CCTCCCTACTTCAATTGATTCGAGTAGACGGAAAGCCATGCCAGATGCC 864
 Qy 241 IleThrGlyArgGlnSerValLeuValProTyrGluProGlnValGlyThrGluPhe 260
 Db 865 ATCACAGGAAAGACAGAAGATGTTGCTGGTACCTTAAAGGCCACCCAGGGTGGACTGAAATTC 924
 Qy 261 ThrThrValLeuThrAspNhemetCysAsnSerSerCysValGlyGlyMetAsnArg 280
 Db 925 ACCACAGTGTGTACAATTCTATGTGTAAACAGCAGTGTGGAGGTGACCCGGT 984
 Qy 281 ProIleLeuIleLeuValThrIleGluThrArgAspGlyGlnValLeuGluArgArgCys 300
 Db 985 CCATTCTTAATCATTTGTTACTCTGGAAACACAGGATGGAACTGGGACGGTGC 1044
 Qy 301 PheGluAlaArgGlyIleCysSerAlaCysProGlyArgAspArgLysAlaAspGluAspSerIle 320
 Db 1045 TTGTAGGGCCGGATCTGGCCTGGACAGTACAAAGAACGGGATGAACTAGATCC 1104
 Qy 321 ArgLysGlnGlyValSerAspSerThrLysArgLysGluLysArgProPheArg 340
 Db 1105 AGAAAGCAGCAAGTTGGACAGTACAAAGAACGGGATGAACTGGGATGAACTGGT 1164
 Qy 341 GlnAsnThrHisGlyIleGluMetThrSerIleLysLysArgSerSerProAspGlu 360
 Db 1165 CAGAACACACAGGTATCCAGACATCAAGAAAGAGATGGAGATGGAGATAAGAG 1224
 Qy 361 LeuLeuIleProValArgGlyArgGluThrTrpGluMetLeuIleLysIleLysGlu 380
 Db 1225 CTCTTATCACTTACAGTGGGCCGCTGAGCTTATGAACTGTTGAATCAAGAG 1284
 Qy 381 SerLeuGluLeuMetGlnIntryleuProGlnHisthrIleGluThrTrpArgGlnGln 400
 Db 1285 TCCCTGGAACTCATGGCACTTCTTCAAGCACAATTCAGCACAATTCAGCAAACGCCAA 1344
 Qy 401 GlnGlnGlnHisGlnHisLeuLeuGlnLysSHisLeuLeuSerAlaCysPheArgAsnGlu 420
 Db 1345 CACAGCAAGCACAGCACTTACTCAGAACATCTCCCTAGCCCTCTGAAATGAG 1404
 Qy 421 LeuValGluProArgArgGluThrProLySglnSerAspValPhePheArgHisSerLys 440
 Db 1405 CTTGGAGACCCCCGGAGAAACTCCAAAACATCTGAGCTTCTCTAGATTCAG 1464
 Qy 441 ProProLysArgSerValTyrPhe 448
 Db 1465 CCCCCAAACCGATCAGTGTACCTCA 1488

RESULT 4
 US-09-606-421B-333
 ; Sequence 333, Application US/09606421B
 ; Patent No. 6531315
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Tongtong
 ; APPLICANT: Pan, Lipun
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Bangur, Chaitanya S.
 ; APPLICANT: Hosken, Nancy
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Ajun
 ; APPLICANT: Skeiky, Yasir A. W.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 ; AND DIAGNOSIS OF LUNG CANCER
 ; FILE REFERENCE: 210121.455C9

Qy CURRENT APPLICATION NUMBER: US/09/606,421B
 ; NUMBER OF SEQ ID NOS: 358
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 333
 ; LENGTH: 2816
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; US-09-606-421B-333

Alignment Scores:
 Pred. No.: 1. 1.13e-250 Length: 2816
 Score: 2383.00 Matches: 448
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-09-670-568C-1 (1-448) x US-09-606-421B-333 (1-2816)

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 Db 145 ATGTCCTAGAACACAGAACAGAACATGATTCTCAGTCAGAGTTTCAGCATATCTGG 204
 Qy 21 AspPheLeuGluGlnProleCybSerValGlnProleLeuSerPheValAspGlu 40
 Db 205 GATTTCCTGGAAACGCTTATGGTCAAGTCAGCCATTGACTGAACTTGTGGATGAA 264
 Qy 41 ProSerGluLysPGL1AlaThrAsnLysIleGluLysSerNetAspCysIleArgGlnGln 60
 Db 265 CCATCAGAAGTGGTCGACAACAGATGAGATAGCTGAGATTCAGTCAGTGCATGCCAG 324
 Qy 61 AspSerAspIleUserAspPheMetTrpProGlnTrpProMetTrpProGlnTrp 80
 Db 325 GACTTCGACCTGAGTACCCATGTGCCAGTACAGTACGAACTGGGCTCTGAAACAGC 384
 Qy 81 MetAspGlnGlnIleGlnAsnGlySerSerSerSerProTyroSerAsnThrAspHisAla 100
 Db 385 ATGGACAGCAGATTAGAAAGCTGTCCTGTCACACAGTCCTATAACAGACCACGG 444
 Qy 101 GlnAsnSerValThrIleAlaProSerProTyroSerThrPheAspAlaLeu 120
 Db 445 CAGAAAGCGGTACCGGCCCTCGCCCTTACCCACCCACCTCCACCTTCGATGCTCTC 504
 Qy 121 SerProSerProAlaLeProSerAsnThrAspIlyProLysSerPheAspVal 140
 Db 505 TCTCCATCACCCGCCCTCCAAACCCGACTACCCGGGACGAGTTTCGCGGTG 564
 Qy 141 SerPheGlnGlnSerSerThrAlaIleSerSerThrAlaIleSerSerThrAlaIle 160
 Db 565 TCCTTCAGCAGTGGAGACCTGGCCACCTGGAGCTTCACTGAACTCAAGTCAAG 624
 Qy 161 LysLentylCysGlnIleAlaLysIleAlaLysIleLysValMetThrProPro 180
 Db 625 AAACCTCTACGCTCCAAATTGCAAAAGACATGCCCATCAGATGCCCACCT 684
 Qy 181 ProGlnGlyAlaValIleAlaLysIleAlaLysIleLysValMetThrGlu 200
 Db 685 CCTCAGGGAGCTGTTCCGGCCATGCCCTCTCAGAAAAGCTGAGCACGTCACGGAG 744
 Qy 201 ValValLysArgCysProAspHisGluLeuSerArgGluPheAsnGlyLeuIleAla 220
 Db 745 GTGGTGAAGCGGTGCCCCAACATGGCTGAGCTGAGTCAGATGAGAAGTCCC 804
 Qy 221 ProProSerHisLeuLeuArgValGluGlyAsnSerHisAlaGlnIleValGluPro 240
 Db 805 CCTCCCTAGTCATTGATTGAGTCAGTGGCTGAGTCAGATGAGAAGTCCC 864
 Qy 241 IleThrGlyArgGlnSerValLeuValProGlnValGlyThrGluPhe 260
 Db 865 ATCACAGGAAAGACGGGTGCTGGTACCTPATGACCCACCCAGGTTGGACTGATTTC 924
 Qy 261 ThrThrValLeuThrAsnSerSerCysValGlyGlyMetAsnArgArg 280

Sequence 333, Application US/09630940B		Query Match:	100.00%	Indels:	0
		DB:	4	Gaps:	0
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Qy	281 ProIleLeuIleLevalThrLeuGluThrArgAspGlyYglValLeuGlyA... 300	US - 09-670-568C-1 (1-448) x US - 09-630-940B-333 (1-2816)			
Db	985 CCATTCTTAATCATGTAATGAAACAGATGGCCAGCNSC 1044	Qy 1 MetSerGlnSerThrGlnThrAspGluProGluValPheGlnHisIleTrp 20			
Qy	301 PheLysAlaArgIleCysAlaCysProGlyArgAspGlyAlaaspGluAspSer... 320	Db 145 ATGTCAGGACAGAACAGAAATGAAATTCTCACGAGGTTCCACCATATCTGG 204			
Db	1045 TTGAGGGCCGGATCTGCTCTGCCAGAAAGAGACAGAAAGGGATGAAGATAGATC 1104	Qy 21 AspPheLeuGluGlnProIleCysSerValGlnProIleLeuGlyAspLeuGlu... 40			
Qy	321 ArgLysGlnGlnValSerAspSerThrLysArgProPheArg 340	Db 205 GATTTCTGAAACGCTATATGTCAGCTAGCCATTGACTTGTCAGTCAGCAG 264			
Db	1105 AGAAAGCAGCAAAGTTTCGCAAGTACAAGAAAGCGCCCTTTCGT 1164	Qy 41 ProSerGluAspGlyAlaLysAspLysIleGluIleSerMetAspCysIleArgMetGln 60			
Qy	341 GluAsnThrHisGlyIleGlnMetThrSerIleLysLysArgArgSerProAspGlu 360	Db 265 CCATGAGATGGTCGAAACAAAGATGAGATTAGCATGGACTATCCGATGCAG 324			
Db	1165 CAGAACACACATGATGTTATCCAATGATCATACTGAAACGAAACGAAAGATCCCAGATGATC 1224	Qy 61 AspSerAspLeuAspAspProMetTrpProGlnTrpThrAsnLeuGlyIleLeuAsnSer 80			
Qy	361 LeuLeutyrLeuProValArgGlyIargGluIthrItyrGluMetIleLeuIlysIleGlu 380	Db 325 GACTGGACCTGAGTCACCCATGGACCTGAGTGGCCACAGTGCCACAGTCAG 384			
Db	1225 CTGTTATCTTACAGTGAGGGGGTGAAGACTATGAAATGCTGTGAAGATCAAAGAG 1284	Qy 81 MetAspGlnGlnIleGlnAsnGlySerSerSerIleSerProTyro... 100			
Qy	381 SerLeuGluLeuMetGlnIleGlyIleGluThrItyrArgGlnGlnGln 400	Db 385 ATGACACGACGAGGTTGACCCATGAGCCCTATACAGACGCCATATACAGACGCCGCG 444			
Db	1285 TCCCTGGAACTCATGCACTGACCTTCCTCAGCACACAATGAAAGTACAGGCAACAGCAA 1344	Qy 101 GluAsnSerValThrAlaProSerProTyro... 120			
Qy	401 GlnglGlnHisIlnHisIleLeuGlnLysIleLeuSerAlaCysPheArgAsnGlu 420	Db 445 CAGAACAGCTACGGGCTCCCTACGACAGCCAGTCACCTCTGATGCTCTC 504			
Db	1345 CACCGAGGACCACAGCACTTACTTCAGAACACATCTCCCTCAGGAACTGAGT 1404	Qy 121 SerDroserProAlaIleProSerAsnThrAspIly... 140			
Qy	421 LeuValGluIproArgArgGluIthrProLy... 440	Db 505 TCCTCATCACCCCGCATCCCTCCAAACCCGACTACCCACGCCACAGCTGGCGGT 564			
Db	1405 CTTGTTGGACCCGGAGAAACTCCAAAACAACTCTGAGCTCTTAGACATCCAAAG 1464	Qy 141 SerPheGlnGlnSerThrAlaLys... 160			
Qy	441 ProProAsnArgSerValtyrPto 448	Db 565 TCCCTTCAGCAGGTCAGGACGCCAGTCAGTACAGTCAAGGTGACCTCACCT 624			
Db	1465 CCCCAAAACCGATCAAGTCACTCCA 1488	Qy 161 LysHeutyrCysGlnIleAlaIleSerH... 180			
Db	RESULT 5	Db 625 AAATCTACTGCCCCATTCAGATAAACACTGCCCCACCT 684			
Qy	US - 09-630-940B-333	Qy 181 ProGlnGlyAlaValIleArgAlaMetProValItyrIlysAlaIgluIleValThrGlu 200			
	Sequence No. 677514	Db 685 CCTCAGGGAGCTGTATCGCGCCATGCTGTCTACAAAAAAAGCTGAGCTGAG 744			
	GENERAL INFORMATION:	Qy 201 ValValLyArgCysProLysHisGlnLeuSerArgGluPheAsnGluGlyIleAla 220			
	APPLICANT: Wang, Tongtong	Db 745 GTGCTGAAACGGTCCCTGAGCTGAGCTGAGCTGAGCTGAGATGCC 804			
	APPLICANT: Fan, Lipin	Qy 221 ProProSerHisIleUleargValGluGlyAsnSerHisIleGlnItyrValGluAspPro 240			
	APPLICANT: Kalos, Michael D.	Db 805 CCTCTCTAGCTATGATTCAGTAGAGGGAAACAGCAGTCATGAGATGCC 864			
	APPLICANT: Bangur, Chaitanya S.	Qy 241 IleThrGlyArgGlnSerValLeuValIleArgValGluIleGlyThrGluPhe 260			
	APPLICANT: Hosken, Nancy	Db 865 ATCACAGGAGAACAGAGTGTGTCACCTTATGAGCCACCCCGACTGATTC 924			
	APPLICANT: Fanger, Gary R.	Qy 261 ThrThrValleutyrAsnSerIleAspGlyMetAsnArgArg 280			
	APPLICANT: Li, Samuel X.	Db 925 ACGACAGCTGTTGACATTCACTGTTGAGCTGTTGAGGGATGAAACCCCGT 984			
	APPLICANT: Wang, Ajun	Qy 281 ProfileLeuIleLeuIleGluGluIleGluGlyIleGluGlyMetAsnArgArg 300			
	APPLICANT: Skeiky, Yasir A. W.	Db 985 CCAATTGTTAATCATGTTACTCTGAAACAGAGATGGAAAGTCGACCTGC 1044			
	APPLICANT: Henderson, Robert A.	Qy 301 PheGluIlaArgIleCysSalicylAspGlyIleGluGlyIleGluGlyMetAsnArgArg 320			
	APPLICANT: McNeill, Patricia D.	Db 1045 TTGAGGGCCGGATCTGCTGAGCTGAGATGAGATGACATC 1104			
	TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY	Qy 321 ArglyGlnGlnValSerAspThrLysAsnGlyAspGlyIleGluGlyIleGluGlyMetAsnArgArg 340			
	TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY	Score: 1.13e-250			
	FILE REFERENCE: 210121_455C10	Length: 2333.00			
	CURRENT FILING DATE: 2000-08-02	Matches: 448			
	NUMBER OF SEQ ID NOS: 367	Percent Similarity: 0			
	PERCENT: 100.00%	Best Local Similarity: 0			
	SOFTWARE: FASTSEQ for Windows Version 3.0	Best Overall Similarity: 0			
	SEQ ID NO: 333	Matched Sequences: 0			
	LENGTH: 2816	Number of Matches: 0			
	TYPE: DNA	Conservative: 0			
	ORGANISM: Homo sapiens	Mismatches: 0			
	US - 09-630-940B-333	10105 AGAAAGCAGCAAGTTGCAAGTACAGTACAGTACAGTACATC 1104			

Qy	341	GlnAsnThrHisGlyIleGlnLeuSerIleLysArgArgSerProAspAspGlu	360	Db	121	CCATGAAAGATGGTTCGACAAAGATGAGATAGCATGGCTATCGGCAATGCG	180	
Db	1165	CAGAACACATGGTATCCAGACAACTCATAGAACAGAATCCCAGATGATAA	1224	Qy	61	AspSerAspLeuSerAspPpMetTrpProDlnTrpThrAsnLeuGlyLeuLeuAsnSer	80	
Db	361	LeuLeuTyrlLeuProValArgGlyArgGluThrTyrGluLeuLeuLysIleLysGlu	380	Db	181	GAETGGACCTGAGTCACCCCATGGCCACAGTAGACGACCTGGGCTCTGAACG	240	
Qy	1225	CTGTATTAACAGTGAGGCCGAGACTATGAAATGCTGTAAGATCAAAGAG	1284	Qy	81	MetAspGlnGlnIleGlnArgGlySerSerSerProTyrrhenthrrAspHisAla	100	
Db	381	SerLeuGluLeuMetGlnTyrlLeuProGlnHisThrIleGluThrTyrArgGlnGlnGln	400	Db	241	ATGGACAGCAGGATGAGACGAGATTCAGACAGACCCATTCTGACGACACGGG	300	
Db	1285	TCCCTGGAACTCATGCACTACCTTCCTCTCACACAATGAACTGACGCAACAGCA	1344	Qy	101	GlnAsnSerValThrAlaProSerProSerProTyrrAlaGlnProSerSerThrPheAspAla	120	
Qy	401	GlnGlnGlnHisGlnHisIleLeuLeuSerIleAlaCypPheArgAsnGlu	420	Db	301	CAGAAAGCTCACGGGCCATCCGGCCCTCGGCCTACCCACACCCAGCTGAC	360	
Db	1345	CAGCAGGACCCAGCCTTACTTCAGAACTCTCCCTCAGCTGCTTCAGAAATGAG	1404	Qy	121	SerProSerProAlaIleProSerThrAspTyrrProGlyProHisSerPheAspVal	140	
Qy	421	IeuaValGluProArgArgGluThrProLyserGlnSerAspValIphePheArgHisSerLys	440	Db	361	TCTCCATCACCCGCCATCCCTCCAAACCCGACTACCCAGGCCACAGTTGAC	420	
Db	1405	CTGTGAGCCGGAGAAACTCCAAAACAACTCTGAGCTCTTAGACATCCAG	1464	Qy	141	SerPheGlnGlnSerSerThrAlaIleSerIleAlaThrPheAspThrGluLeuIlys	160	
Qy	441	ProProAsnArgSerValtyrPco	448	Db	421	TCCCTCAGGATGTCGACGCCAACGCTGGACGTATTCCACTGAACTGAG	480	
Db	1465	CCCCAACACGATCAGCTACCCA	1488	Qy	161	LysLeuTyrcySGlnIleAlaLysIleSerIleAlaLysValMetThrProPro	180	
Db	RESULT 6							
Qy	US-09-643-597-337							
;	Sequence 337, Application US/09643597							
;	; Patent No. 626072							
;	GENERAL INFORMATION:							
;	; APPLICANT: Wang, Tongtong							
;	; APPLICANT: Fan, Liqun							
;	; APPLICANT: Kalos, Michael D.							
;	; APPLICANT: Bangur, Chaitanya S.							
;	; APPLICANT: Hosken, Nancy							
;	; APPLICANT: Fanger, Gary R.							
;	; APPLICANT: Li, Samuel X.							
;	; APPLICANT: Wang, Aijun							
;	; Skeiky, Yasir A. W.							
;	; Henderson, Robert A.							
;	; APPLICANT: McNeille, Patricia D.							
;	TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY							
;	TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER							
;	FILE REFERENCE: 210121_455CL1							
;	CURRENT APPLICATION NUMBER: US/09/643,597							
;	CURRENT FILING DATE: 2000-08-21							
;	NUMBER OF SEQ ID NOS: 369							
;	SOFTWARE: FastSEQ for Windows Version 3.0							
;	SEQ ID NO: 337							
;	LENGTH: 1551							
;	TYPE: DNA							
;	ORGANISM: Homo sapiens							
;	US-09-643-597-337							
;	Alignment Scores:							
Pred. No.:	2.21e-229	Length:	1551	Qy	321	ArgLysGlnIleSerAspSerThrLysAsnGlyAspGlyThrLysArgProPheArgProPheArg	340	
Score:	2185.00	Matches:	416	Db	961	AGAAAGCAGCAAGTTCGAGTCAGAACTGAGCTTACGGAGCCGTTTCGTT	1020	
Percent Similarity:	94.80%	Conservative:	3	Qy	341	GlnAsnThrHisGlyIleGlnMetThrSerIleLysAspArgSerProAspAspLys	360	
Best Local Similarity:	94.12%	Mismatches:	7	Db	1021	CAGAACACATGGTACCATGAGTCATCAACAAACGAGATCCCAAGATGAGCA	1080	
Query Match:	91.69%	Indels:	16	Db	1021	CGAGACACATGGTACCATGAGTCATCAACAAACGAGATCCCAAGATGAGCA	1080	
DB:	3	Gaps:	1	Db	1021	CGAGACACATGGTACCATGAGTCATCAACAAACGAGATCCCAAGATGAGCA	1080	
;	US-09-670-568C-1 (1-448) x US-09-643-597-337 (1-1551)							
Qy	1	MetSerGlnSerThrGlnThrAsnGluHeLeuUserProGluValPheGlnHisIleTrp	20	Qy	361	LeuLeuTyrlLeuProValArgGlyArgGluThrTyrGluMetLeuLeuIleGlu	380	
Db	1	ATGGCCAGAGACACAGAACATGAAATGCTCAGTCAGAGCTTCAGATTCAGATTC	60	Db	1081	CTGTATTACTTACCGTAGACTCATGAGCTTCTCAGCTTACGAAATGCTGTGAAGATCAAAGAG	1140	
Qy	21	AspPheLeuGluGlnProIleCysSerValGlnProIleAspLeuAspPheValAspGlu	40	Qy	381	SerIleGluLeuMergInTrpLeuProGlnHisIleGluGlyIleGluGlyGlnGln	400	
Db	61	CATTCTCTGAAACAGCTTATGTCAGTCAGCTTACCTTCAGACAACTTCAGCTTAC	1200	Db	1141	TCCCTGGAACTCATGAGCTTCTCAGCTTACGAACTTCAGCTTACGAACTTCAGCTTACGAA	1200	
Qy	41	ProSerGluAspIleAlaThrAsnLysIleGluIleSerAlaCysPheArgAsnGlu	60	Qy	401	GlnGlnGlnHisIleLeuLeuSerAlaCysPheArgAsnGlu	420	
Db	1201	CAGCAGCAGACCAAGGACGACACTTCAAGGAGACAGGAGACAGGAGACAGGAGAC	1230	Db	1201	CAGCAGCAGACCAAGGACGACACTTCAAGGAGACAGGAGACAGGAGACAGGAGAC	1230	

Qy	421	LeuValGluProArgArgGluThrProLysGlnSerAspValPhePheArgHisSerLys	440
	1231	-----CGACCTCAATACAGTCATCTCATATGGTAACAGCTCC	1272
Qy	441	PROPO	442
Db	1273	CCACCT 1278	
RESULT 7			
US -09-542-615A-337			
; Sequence 337 Application US/09542615A			
; PATENT NO. 6518256			
; GENERAL INFORMATION:			
; APPLICANT: Wang, Tongtong			
; APPLICANT: Pan, Lijun			
; APPLICANT: Kalos, Michael D.			
; APPLICANT: Bangur, Chaitanya S.			
; APPLICANT: Hosken, Nancy A.			
; FANGER, Gary R.			
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY			
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER			
; FILE REFERENCE: 210121_455CB			
; CURRENT APPLICATION NUMBER: US/09/542 615A			
; CURRENT FILING DATE: 2000-04-14			
; NUMBER OF SEQ ID NOS: 350			
; SOFTWARE: FastSEQ for Windows Version 3.0			
; SEQ ID NO 337			
; LENGTH: 1551			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
US -09-542-615A-337			
Alignment Scores:			
Pred. No.:	2.21e-229	Length:	1551
Score:	2185.00	Matches:	416
Percent Similarity:	94.80%	Conservative:	3
Best Local Similarity:	94.12%	Mismatches:	7
Query Match:	91.69%	Indels:	16
DB:	4	Gaps:	1
US -09-670-568C-1 (1-448) x US -09-542-615A-337 (1-1551)			
Qy	1	MetSerGlnSerThrGlnThrAsnGluPheLeuSerProGluValPheGluHisIleTrp	20
Db	1	ATGTCCTAGAGAACAGCAATGAAATTCTCAAGGTTTCCAGATAATCTGG	60
Qy	21	AspPheLeuGluGlnProLysSerValGlnProLeuAsnPheValAspGlu	40
Db	61	GATTTCTGGAAACAGCCTATATCTTCACTTCAAGGCCATTGACTTGAAACTTGTGGATGAA	120
Qy	41	ProSerGluAspPheAlaThrAsnLysIleGluLeSerMetAspCysIleArgMergln	60
Db	121	CCTATGAGAGATGGTGCACAAACAGTTGAGATTAACGTTGACTGATCCATGCG	180
Qy	61	AspSerAspLeuSerAspProMetTrpProGlnTyrrhAsnLysIleLeuAsnSer	80
Db	181	GACTCGGACCTGAGTGAACCCATGGCCACACTACAGAACTGGGCTCTGAAACRG	240
Qy	81	MetAspGlnGlnIleGlnAsnGlySerSerSerThrProtyrAsnThrAspHisAla	100
Db	241	ATGGACCAAGCAATTGAAACGCTCCMGTGACCACTGTCACCCATACAGAACCG	300
Qy	101	GlnAsnSerValThraAlaProserProtyrAlaGlnProSerSerThrPheAspAlaIeu	120
Db	301	CAGAACAGCTGCTACGGGCCCCCTGGCCCTAGGACAGCCAGTCACCTTCATGCTC	360
Qy	121	SerProSerProAlaIleProserAsnThrAspTrpProGlyProHisserPheAspVal	140
Db	361	TCTCCATCACCCCATCCCTCAACACGGACTACCCGGCACAGTTTCGACG	420
Qy	141	SerPheGlnGlnSerSerThrAlaIlysSerAlaIlysSerAlaIlysSerAlaIlys	160
RESULT 8			
US -09-606-421B-337			
; Sequence 337, Application US/09606421B			
; GENERAL INFORMATION:			
; Patent No. 6531215			
; APPENDIX: Wang, Tongtong			
; APPENDIX: Fan, Lijun			
; APPENDIX: Kalos, Michael D.			
; APPENDIX: Bangur, Chaitanya S.			
; APPENDIX: Fanger, Gary R.			
; APPENDIX: Hoben, Nancy S.			

Alignment Scores:											
Pred. No.:	Score:	Length:		Matches:		Percent Similarity:		Best Local Similarity:		Query Match:	
US-09-670-568C-1 (1-448) × US-09-630-940B-337 (1-1551)		Length: 1551		Matches: 416		Percent: 94.80%		Conservative: 3		Best Local Similarity: 94.12%	
DB: 4		Indel: 8:		Mismatches: 7		Gaps: 1		Query Match: 91.69%		DB: 1	
Qy 1 MetSerGlnSerThrGlnThrAspGluPheLeuUserProGluValPheClnHisIleTyr 20		Length: 2185.00		Matches: 2185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Db 1 ATGCCCCAGCAAGCAAAATGAATTCAGTCAGTCCAGGGTTTCCAGCATATCTGG 60		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Qy 21 AspPheLeuGluLysInProleCysSerValGlnProleLeuAsnProValLeuAspGlu 40		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Db 61 GATTTTCGGAACAGCTTATAATGTTCACTGACTGCCATTGACTGAACTTGTGATGAA 120		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Qy 41 ProSerGluAspGlyAlaThrAsnLysIleGluIleSerMetAspCysIleArgMetGln 60		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Db 121 CCATCAGAAGATCGGCACAAAACAAGATGAGATTAGATGGATTGATCCGATGAG 180		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Qy 61 AspSerAspLeuUserAspProMetTrrPrglolyTrThrAsnLysIleGluIleAsnSer 80		Length: 2185.00		Matches: 2185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Db 181 GACTCGGACCTGACTGACCCATGTCGGCAACAGTACACCAACCTGGGGTCTGAAACG 240		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Qy 81 MetAspGlnLysIleGlnAsnGlySerSerThrSerProTyrsAsnThrAspHisAla 100		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Db 241 ATGGACCAGCAGATTCTAGAACGCTTGACGAACTGAGCTGGTCTCTGCTCCATAACAGACCACCG 300		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Qy 101 GlnAsnSerValThrAlaProSerProTyraGlnInProSerSerThrPheAspAlaLeu 120		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Db 301 CAGAACACGGCTCAGCCAGCTGGCCTACGCAAGCTCCACCTTGTGTCCTGC 360		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Qy 121 SerProSerProAlaLeProSerAsnThrAspTyPrglolyProHisSerPheAspVal 140		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Db 361 TCTTCATACCCCTCACCCATCCCTCAAACACGGACTCCAGGCCACAGTTGCACTG 420		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Qy 141 SerPheGlnGlnSerSerAlaLysSerThrAlaLysSerAlaLysSerThrGluLeuLys 160		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Db 421 TCTTCATCAGCAGTCTGAGCACTGGCACCCTGAGCTGAACTGATTCCACTGACTGAG 480		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Qy 161 LysLeuTyrCysGlnIleAlaLysThrCysProleGlnIleLysValMetThrProPro 180		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Db 481 AAACTCTACTGCCAATTCGAAAGACATGCCCATCCGATCAAGCTGATGCCCACT 540		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Qy 181 ProGlnGlyAlaValIleArgAlaMetProValItyrLysAlaGluHisValThrGlu 200		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Db 541 CCTCAGGGAGCTTATCGGCCATGCTGTCATAAAAGCTGAGCTGACGGTCACTG 600		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Qy 201 ValIvalysArgCysProAsnHisGluLeuUserArgGluPheAsnGluGlyIleAla 220		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Db 601 GTGGTGAAGGGTGGCCCAACCTGAGCTGAGCTGACGGAGCATGTC 660		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Qy 221 ProProSerHisIleLeuIleArgValGluGlyLysAsnSerHisIleAlaGlnItyrV 240		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Db 661 CCTCCCTAGTATTGATTGAGTAGAGCTGAGCTGCCCAGTATGAGATGCC 720		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Qy 241 IleThrGlyArgGlnSerValIleLeuIleArgValGluProGlnValGlyIleGluPhe 260		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Db 721 ATCACAGGAAGACAGATGCTGTTACCTGATGAGCTGAGCTGAGCTG 780		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Qy 261 ThrThrValLeuThrAspPheMetCysAsnSerHisGluLeuUserArgGluGlyIleAla 280		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Db 781 AGCACAGCTCTGTAACATTGATGAGCTGACGGAGTGTGTCAGGGATGAGATGCC 840		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Qy 281 ProIleLeuIleLeuIleArgValGluIleArgGlyGlnValLeuGlyIleArgGlyCys 300		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
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Qy 341 GluAsnThrHisGlyIleGluLeuUserArgGluGlyIleAspGluLeuAspSerIle 332		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Db 342 ArgLySGLngInValLeuUserArgGluIleArgGlyIleAspGluLeuAspSerIle 332		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Qy 381 SerLeuGluLeuMetThrGlyIleArgGluIleLeuUserArgGluIleArgGlyIleAsp 332		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Db 382 SerLeuGluLeuMetThrGlyIleArgGluIleLeuUserArgGluIleArgGlyIleAsp 332		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Qy 383 SerLeuGluLeuMetThrGlyIleArgGluIleLeuUserArgGluIleArgGlyIleAsp 332		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Db 384 SerLeuGluLeuMetThrGlyIleArgGluIleLeuUserArgGluIleArgGlyIleAsp 332		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Qy 385 SerLeuGluLeuMetThrGlyIleArgGluIleLeuUserArgGluIleArgGlyIleAsp 332		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Db 386 SerLeuGluLeuMetThrGlyIleArgGluIleLeuUserArgGluIleArgGlyIleAsp 332		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Qy 387 SerLeuGluLeuMetThrGlyIleArgGluIleLeuUserArgGluIleArgGlyIleAsp 332		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Db 388 SerLeuGluLeuMetThrGlyIleArgGluIleLeuUserArgGluIleArgGlyIleAsp 332		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Qy 389 SerLeuGluLeuMetThrGlyIleArgGluIleLeuUserArgGluIleArgGlyIleAsp 332		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Db 390 SerLeuGluLeuMetThrGlyIleArgGluIleLeuUserArgGluIleArgGlyIleAsp 332		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Qy 391 SerLeuGluLeuMetThrGlyIleArgGluIleLeuUserArgGluIleArgGlyIleAsp 332		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Db 392 SerLeuGluLeuMetThrGlyIleArgGluIleLeuUserArgGluIleArgGlyIleAsp 332		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Qy 393 SerLeuGluLeuMetThrGlyIleArgGluIleLeuUserArgGluIleArgGlyIleAsp 332		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Db 394 SerLeuGluLeuMetThrGlyIleArgGluIleLeuUserArgGluIleArgGlyIleAsp 332		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Qy 395 SerLeuGluLeuMetThrGlyIleArgGluIleLeuUserArgGluIleArgGlyIleAsp 332		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Db 396 SerLeuGluLeuMetThrGlyIleArgGluIleLeuUserArgGluIleArgGlyIleAsp 332		Length: 9185.00		Matches: 9185.00		Percent Similarity: 94.80%		Best Local Similarity: 94.12%		Query Match: 91.69%	
Qy 397 SerLe											

SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 332
; LENGTH: 2270
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-630-940B-332

Aligned Scores:
; Pred. No.: 4.16e-229 Length: 2270
; Score: 2185.00 Matches: 416
; Percent Similarity: 94.80% Conservative: 3
; Best Local Similarity: 94.12% Mismatches: 7
; Query Match: 91.69% Indels: 1.6
; DB: 4 Gaps: 1

US-09-670-568C-1 (1-448) x US-09-630-940B-332 (1-2270)

Qy 1 MetSerGlnSerThrGlnThrAsnGluPheLeuSer-ProGluValIleGlnHisIIleTrp 20
Db 145 ATGTCCAGGCCACAGCAAAATGATTCTCAGGGTTCCAGCATTCCTGG 204

Qy 21 AspPheLeuGluGlnProIleCysSerValGlnProLeuSerPheValAsnGlu 40
Db 205 GATTTCCTGGAACAGGCTATAATGTTCAAGTCAGTCAGCCATTGGATCAA 264

Qy 41 ProSerGluIaspGlyAlaLysAsnLysIleGluIleSerMetAspCysIleArgMetGln 60
Db 265 CCATCGAAAGATGGTGCAGAACAGATTGAGATTAGCATGGACTGTATCGCATGZG 324

Qy 61 AspSerAspLeuSerAspProMetIleProGlnTyrThrAsnLeuAsnSer 80
Db 325 GACTCGACCTGAGTCACCCATGTGCCACAGTAACGAACTGGGCTCTGAACGC 384

Qy 81 MetAspGlnGlnIleGlnAsnGlySerSerSerThrSerProTyro239ThrAspHisAla 100
Db 385 RTGGACCACGAGGATTCAGAAAGGGCTCTCGTCCCACAGTCCTATCACAGACCAGCG 444

Qy 101 GlnAsnSerValThrAlaProSerProTyro239ThrAspHisAla 120
Db 445 CAGAAAGGTCACGGGCCCTCGCCCTACGCCAGCTCCACAGCCACAGCCACAGCA 504

Qy 121 SerProSerProAlaLeProSerAsnThrAspPTyrProGlyProHisSerPheAspVal 140
Db 505 TCTCCATCACCCGCCATCCCTCCACACCCACTACCCAGTCAGTGCTGCTG 564

Qy 141 SerPhagGlnInSerSerThrAlaLysSerAlaThrTrpThrSerThrGluLeuLys 160
Db 565 TCCCTTCAGAGTCAGTCAGGCCAGTCGCCACCTGGAGTATTCACACTGAG 624

Qy 161 LysLeutYrcGlnIleAlaLysThrProValTyrLysSylLeuHisValThrGlu 200
Db 625 AAACCTACAGCCAAATGCAAGACATGCCACATGCAAGTCAGTGCACCCACCT 684

Qy 181 ProGlnIlyalavaleArgAlaLeuSerAlaLysLeuSerAlaLysLeuHisValThrGlu 200
Db 685 CCTCAGGGAGCTGTATCCGGCCATGCCCTGCTCATCAAAGCTGAGCTCACGAG 744

GENERAL INFORMATION:
APPLICANT: wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Hosken, Nancy
APPLICANT: Panger, Gary R.
APPLICANT: Li, Samuel X.
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121-455C10
CURRENT APPLICATION NUMBER: US-09-630-940B
NUMBER OF SEQ ID NOS: 367
CURRENT FILING DATE: 2000-08-02
NUMBER OF SEQ ID NOS: 367

RESULT 13
Sequence 3-0-9-630-940B-332
Patent No. 6737514
GENERAL INFORMATION:
APPLICANT: wang, Tongtong
APPLICANT: Fan, Liqun
APPLICANT: Kalos, Michael D.
APPLICANT: Hosken, Nancy
APPLICANT: Panger, Gary R.
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121-455C10
CURRENT APPLICATION NUMBER: US-09-630-940B
NUMBER OF SEQ ID NOS: 367
CURRENT FILING DATE: 2000-08-02
NUMBER OF SEQ ID NOS: 367

745 GTGGTAAGGGTGCCCCAACCATGAGCTGAACTCAACAGGGACAGATTGCC 804
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925 ACGACAGTCAGTGTGAGATTCACTGTTGGGGATGAAACGGCCGT 984
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985 CCAAAATTTCATATCATTGTTTACTCTGTTAACCTGAAACAGAGTGGCTGC 1044
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Mon Oct 3 14:27:28 2005

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Search completed: October 3, 2005, 06:06:48
Job time : 283 secs